

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
CCTTGGTGCACCCACACCATTGCTGGCTGCAAGAGGCTGGTGTGTCCTCCGGACACATCTCTTAGG
GTTTTCACCCAGCTTTTACATGACGGCTCCCTGGTTGTGAAGAAATTCATCACAGAAGATCA
ATGCGCTGTAAACACCTTAGCAGGGAATATGCCACCAAAACAGAATAATGGGAATCCGGCGGTGGGA
GAACTGGCCACAGAACTCAAAGAGGAGCAGCATTTGAACCATCGATGGAAAAAATATTTAAATTT
GATCAGATGGGAAGATGGTTTGTGTGCTGGAGGGCTGCTGTGTGTTCTGGAGCATTTGTGCTT
CTATGGCTTGGGACTGCTAATGAGATTGGAGCATATGAAAGAGGCTGTAATTTGGCCCTCAGT
TTGTCAAGGATGAACATTCATCCACTATATGTACTTGACAGGGAGTATGGTTTAAACGCT
TTGTCTGCCATAGCAATCAGCAGAACCGCTTGTCTCATGAACCTTCATGATGAGAGGCTCTTG
GGTGACAATTTGGTGTGACCTTTGACGCATGGTTGGAGCTGGAAATGCTGGTACGATCAATAC
CATATACGACGAGCCAGCCCAAGCCATCTTGGCTGGTGTGCTACATCTTGGTGTGATGGGT
GCAGTGGTGGCTCCTCTGCACAAATATGAGGGGTCCTCTTCTCATCAGAGCTGCATGGTACAC
AGCTGGGATCTTGGGAGGACCTCCACTGTGGCCATGTGTGCCCCAGTGAAAAGTTTCTGTA
ACATGGGTGCACCCCTGGGAGTGGGCTGGGCTCGTCTTGTGTGCTCATTTGGGATCTATG
TTTTCTCCACCTACACCGCTGGCTGGTGCCACTCTTTTACTACGTGGCAATGTACGGTGGATT
AGTTCTTTTTCAGATGTTCTTCTGTATGATACCCAGAAGTAATCAAGCTGCAGAGATAT
CACC AATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATGTACATGGAT
ACATTTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGTGGAGCCACAGAAAATG
AAGAGTCAGCTTCTGGCTTCTGCTCATACAAATATCTGTTTAAATGGGCGAGATATGC
ATTTAAATAGTTTGTACAGACGCTTCTGTTGAAGTTTGAAGATAAGAAACATGTTCATCATAT
TTTAAATGTTCGGTAATGTGATGCTCAGGCTGCCTTTTTCGTGAGATAAATGCGAT
AATCCCTGCCAAATAAGCACACATTTTCAATCTCATGTTTGAAGTATTTTAAATGTT
TTGGTGTAATGTAAACACTAAAGTTTGTGTCATGAGAATGTAGTCTTTTTTACTTTAAAAA
TTTAGTAGGTTCTACTGAGTAACATAAAATTTAGCAAACTGTGTTCATATTTTTTGGAGT
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTGGTAAGGGACAGAGAGAAG
GAGTCACTCGAGCTGTTTGGTTTTTAAATACATAGAACCTTGGACCTTGTTGTATGATTA
GTGAGGAGCCAGTAAGAAACATCTGGGTAATTTGAAACCAAGTGGCTATGTTACATTCATTT
GCTGAACTTACAAAACCTGTTTCATCTGAAACAGGCACAGGTGATGCATCTTCTGCTGTG
CTTCTCAGTGCTCTTCTTCCAAATAGATGTGGTTCATGTTGACTGTGCAGAAATGTTAATC
ATACAGAGAATCCTTGATGGAATTTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
ATAACTTTTAAACATATTTCTACAGAGAAAATATCAAGCATGAAATATGTGCTTTTTCCAG
AATACAAACAGCATACATCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCTCCGCTTCTGCAT
CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGGCCGGTCTGTGAGGG
GGTCCGCGACGGGAGTTCGGCGGCTTGTGTCATCTTGGCTACTGTGGGTCGCAAGATGTCGG
ACATCGGAGACTGGTTTCAGGAGCATCCCGCGCATCAGCGCCTATTGGTTTCGCGGCCACGCTC
CGCGTGCCCTTGGTCCGCAAACTCGGCCTCATCAGCCGCGCATACCTCTTCCCTCTGGCCCGA
AGCCTTCCCTTTATGCTTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTTCCCTGTGG
TGCCAGGAATCGGATTTCTTTATTTGGTCAATTTATATTTCTTATACAGTATTTCTACGCGA
CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCCTCTTAACTG
GATTTGTCATCGTGATTACTGGCTTAGCAATGGATATGCAGTGTGCTGATGATTCCTCTGATCA
TGTCAGTACTTTATGCTCTGGGCCAGCTGAACAGAGACATGATTTGATCATTTTGGTTTGGGA
ACACGATTTAAGGCCTGCTATTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTGTACCGCTGG
CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCTCTGTAGCATGAGGCGAGC
TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGCGCAGGGCTTCCAGTTGGAGACC
AGTGAAGGGCGGCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTTG
CACTTAAACACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACATGAATGTAGTCTTTTC
AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAATATAAGTGTCCACAGTTTTCACGAT
TCTCACTCAAGTCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGCAAACTGAC
TACATTTTTTGGTGTCTTCTCTCTCCCTTTCCGCTGCAATTAATGGGTTTACGGGGTCTCT
AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCT
TCTTGACACATGCTCTCTCCCACTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
CCCAATAAATTGCTCTGCCCTTGACAGGTTCTGTATTATTGACTTTTCCCAAGGCTGGTG
ACAACAATCATATTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGCGGGAG
AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCACTGACATCCCTTTGT
AACCGTTTGGCCACTCTTCAGATATTTTTATAAAAAAAGTACCACGTAGTTTCATGAGGCCA
CAGATTTGGTTATTAATGAGATACGAGGGTTGGTGTGGGTGTTTGTTCCTGAGCTTAAGTA
TCAAGACTGTAGTGGAGTTGACGTAAACATGGGTAGGTTTAAACATGGGGGATGCAACCC
TTTGGCTTTCATATGTAGCCCTACTGGCTTTGTGAGCTGGAGTAGTGGGTTGCTTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTGGAGAGGTCTGGGCATTG
ATTCCCAATTTCAATCTCATTTCTGGATATGTGTTCAATGAGTAAAGGAGGAGACCCCTATA
CGCTATTTAAATGTCACTTTTTGGCTATCCCGGTTTTTGGGTGATGTTCAATTAATCTG
GAGGAAGCGCAGCTCCTCTCTGACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAAATCATTTGGGTTTGGGGTGTGTTA
TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACAGCTTAAATACCCACACCTTTTTT
TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAAACAAATAAAGTTTTTGAAGGCCA
GGCTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
ATTGAGTGGCTGTACACTTTTGGGCACTAAAAGGCTTCAAAGCTTTTGATCAGTTTCTT
TTCAGGAAACATTTGGCTCTAACAGTATGACTATCTTTCCCACTCTTAAACAGTGTGAT
GTGTGTTATCTTAGGAATGAGAGTTGGCAAAACACTTCTCATTTGAAATAGAGTTTGTGTG
TGTGTTCCATATTTAATTTATATGATAAAATAGGTGGCGAGAGTCTGAACCTTAAGTGTCA
TGTTTTGTGTTTCACTGTGGGCCAATAAAGTTTACTGTAAAATTTTAGAGGCCATTACT
CCAATATGTTGACGTACACTCATTTGTACAGCGCTGGAGACTCATTTGATAGTATAAGAATA
TTTCTGACAGTGAAGTACCCGGAGTCTCTGGTGTACCTCTTACAGTCAGCTGCCTGCGAG
CAGTCAATTTTTTCCAAAGGTTTACAAGTATTTAGAAGTTTTCAGTTGAGGCAAAATGTTTC
ATGAAGTTATCTCTTAAACATGTTTAGGAAGCTGATGACGTTATGATTTTGTCTGGATT
ATGTTTCTGGAATAATTTTACAAACAGCTATTTGAGTTTGTGACTTGACAGGCAAAACA
TGACAGTGGATTCTTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTCCC
TTTTGTAAACTAATCCTTTTTATTGGTAAAAAATGTAAATAAATGTGCACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTCGATTAAC TGGTTG
STAGCTTCTATCCTGGGGGCTGAGCGACTCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTTGCGCCAAAGGCTTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCTTGCC
CCTTTGGGGCGGGATGGCTGCGGAAGAAGAGACGAGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCCTACTTGGACTTTGTGGAACGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGCTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTTTGCAAAGACCCATACATCAGAGGC
CATTTTGCAACCTGTGTTGGCAGCAGCAAGATTTTACTATCTTTAAAGCAATGATGCTCCAGA
AAAACATTGAAATGCAGCTGCAGCCATTGCAATTAATTCAAAGAGAAATGGTGTAATTACCT
GACTGCTTAACCGATGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAACTCT
GAGGGAAGTTCCTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAACAGAAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTCCTCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAAGGTCTGAAACTTCCTCCCTCC
CACAAAAAGGCCTGAAGATTCTTGCTTAGAGCATGCAGCATTTGAAGGACCAATAGCAAAC
TTATCAGTACTTTGGAACAGAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
CAAACTACTATAAGAGGAGATTGCTTGCAAGAGAACTCAAGAAGAAGTTATTAATAAGTA
ATAATTAAAGCAATTTAACAAAATGGAAGTTCAAAATTGCTTTAAAAATAAATATTATTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAAATGGTGATTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTCGCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAAATAAAAAAC
 AGTGGAAATGGGAAAAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTTTGCAACAATGTATAC
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGTGT
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATTTCTGATTTTCATGAAGTGGTCCATTCTGCGCT
 TTCTTTATTTCTGGATAACTTGATTGCTTCTCTATGTCCTGTCCATCTTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGTGAA
 GAGGCGCTAAACCTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCAGCATGCC
 TTTTTAGCCCTTCCAATTTCTGCGCTTCTTTTCAAGAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGGTTTTTCAGTC
 ACATCCGCTCTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACCTGAAGGAGGGGAACAGCTCAGTGAAGGCATCTTCATACA
 GAACAGCAAACTCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCTTCAGAGGA
 GTAACCGTGATCAGATTAGAAGTGTGGATTTTTTTATGCGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCAGGGGCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTTACCAGTGTCTATTATCACAACAGTGTCTGTCTGG
 TCTTTGACTTTCAGGCCCTCCCTGGAATTTTTCTTGGAGGCCCATCAGTCCCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 CCTCTCTGAACTTATTTTACATTTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTTAGCTATAGCTTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAGT
 CTTCCCTTTTAAACATTATAAAGCTAGGTTGTCTCTGAAATTTTGAGGCCCTAGAGATAGT
 CATTTTGCAGATGAAGAGCAACGGGACCCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAATATTTTGTCTGAAGAGCAGT
 TTCTCAGACACAACATCTCAGAAATTTAATTTTTAGAAATTCATGGGAATTTGGATTTTTGT
 AATAATCTTTTGTGTTTTTAAACATTTGGTCCCTAGTCACCATAGTTACCAGTCTGTATTTTA
 AGTCAATTTAAACAAGCCAGCTGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAATATTACATTTTGGAGAATAAGAGGGCACTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAACTATAC
 CAGATTGTGCTGAAGTGTGCTTAGGAATTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACACATGTTGACTTTTAACTAGTATGTAAATATTAATCTCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTACACTTAAAGAGTGCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAAAACAAAAGTGACTTGTCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGCCCTGTATGTTTACAGACTCCATACTGTAATATGAGCTTTATGGTGT
 CATTTCTCAGAAACTATACATTTCTGCTCTCCTTCTCCTTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG
 GTGGAAATTTGTAAATAAAAATAATTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLI VFYVLSYLQ PAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
 TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCCTATACCTACTGTAGCTTCTCCAC
 GTATGGACCTAAAGGCTACTGTCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
 GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAaaaaaacagtggaaatggaa
 AAACAGTGTCTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
 TGCCATATTCTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
 AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
 TTCTGTGTGCTTGTGTCACTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
 TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
 TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC
 TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
 CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
 CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGCGCGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGACAGAGGAGCAT
 CCCGTCTACCAAGTCCCAAGCGCGTGGCCCCGCGGTCATGGCCAAAGGAGAAGGCGCGGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCACAAAGCTTTGTCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTGGATGGTGGCTCAGGTGGGCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCTATGGCTACTTCCCTC
 ATCTGGTTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT
 CTTTGAACAATGGTCACTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCCTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAAACCATACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCATCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCACGAGCTG
 AGCCAATCGCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCATACATCAAACTT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTTATGCTGGTGGAGGGGAACCTTTGTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCGTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTACCAAGTTTGCCTCTGGAGTGTC
 ACTGGGCATTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATTGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGCGGCAGATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGACTCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTGCAGTGTCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCACAGGACACTTGGTGTGCTCACTGTGGGGCGGCTGCTCTG
 TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAAGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTATTTTCATAAAAGCTGGAAAGC

MMLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHSTARPIGTCFCSIASLKQSVSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANTHTGTTSHRETQKAYLLAAGVIVICIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMShGPYIKLITGFLTSLAFMLVEGNFVLFCT
YTLGRNEFQNLLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAFLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFTTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

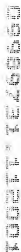
GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGTCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGACTTGGAATACTGAGTTGTTTAGG
ACTTTCATTTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTTCCTACCAAATG
CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLSRDI



CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCACAAAAGCTAATTGAGTACACGTTCTCTGTTGAGTACA
CGTTCTCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTTCAGCAGAAGCCCTACGTTCTTCCCTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGTCAGTAACACT
CCACCATATGAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCGCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCGGCTGCAC
 CTTTCCCTTGTACTTGCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCTCTGAATGTTTTAGCTGGTGCCT
 TGTCTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTCTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCTCTGTGT
 GCAGACAGGGTCCATCTGTCAACCCCTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCTGGAACCCCTATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCTCTAAAGCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGTGGCTCACGCCTGTAATCCAGCACCTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRRLGSTEAGGRSLWFPSDLAE LRELSEVLREYR
 KEHQAYVFLFCGAYLYKQGF AIPGSSFLNVLAGALFGPWLGLLLCCVLTSGATCCYLLSS
 IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCAGTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTTC
 AGCATTTTTTGTGCCAGTACCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGTGCTTTCTGAGCGGTGGTTCCTTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTCACTCACCTGCCATTTCCAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCTTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCACTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAA

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FIGURE 21

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGGG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

CCACGCGCTCCGCCCATCGCTCGGCTGAACCCCTTCTTTGGAGTACGACAGTGTAGG
CAGGGTCCCCACTTGCAGCTCGCAGCAGCTGCAGCAGCTGAGGCGTGTCTGGCTGTG
CCACTGGTGGCGACCGTGTCTAGACGCTGCCATGATGAGCGCTGAGGCGTGCATGTGGGAGTCC
CTCCCTGCCACCCCAATGGCAGCCCACTTCTTTGAAGACTTCAGGCTTTTGTGCCA
CACCCGAATGGGCGCACTTCATCGACAAGCAAGGTACGCCAACCAATGTTCCCACTTCAAATG
GATACGATGTCTAAGAGCCACGACATTTGTTCAGGTTTCTTGGAAATGCTTGTAGCATGCT
TATGAGCACTGGGCGAGCGGCGCAGTTGGAGTCGCGCCAGAGTCTGTGGGCGCTTCAGGAG
TGGTGTCTGAACACTCGGCAGAGGCGGGCGCGCTTGAAGGGGTACGCTACACGGCAGTGTCT
AAGCAGCAGGCAACGACGACATCTTATGGCCCTGTGTCACTGGGGGGCGCTGTGGCGGCAGCT
CGCCAGCCCATTTGGGGCGCTGGGGCGCTGAGGACACATCCCATCCCCGCTGGAACCTGTCC
CGCGCAGACATATTTACGCAATGCGTCTGAAGCTGGTGGCCCAACTCATCTTCAGCCTCA
CTGGAAGCCAGCGCTCTCCGAGACAATCTTGGGTGAGGTTTCCCTGCACACCACCCAGGAGG
CTCATGCTCTTGGCAGTGAACAAAGAGGCCAAGGTAGCACCCCAACCGAGTGTCTCGAGG
AGGACAGCCTCGGCGAGGACAGCACTGGCTGAGCTGGAGACCCCGATGGAGGCGAGCAATCT
GATGAGCAGCGTGAAGAAGCTGTGTCTGTGGCGCAGTGGCAGCTGGTGAAGTGTGGCGGT
GGTCCACAGGGGTCTCGGAAGTCAACCCACAGAAATGTATACTTACATGGCAGCACTGAGC
CGCTGGAACCCGAGGAGGGCATCGCGTATGATTTCCGGCGCCCATGGCCAGCTCGGTGAG
GTCCACCTGCGGCGTTTCAACTCGCCGTTTGAGCACTTGAGCTTCTCTTATCGATCAGG
CAACTACTTCTCAACTTCCATGCAAGTTGGGACAGACCCCAAGTCTCATCTCTGATCCGA
CTCCGAGACCCAGCGCTGGCCCCATCCCCACCCATACCCAGGTCAGGAACCAAGGTTACTGCT
TGGCTCTCTGCGCTACGGCGCCCTCTTAAGGCTACCTAAGCAGGCGCTCCCCCAGGAGAT
GTGCTGCGCTCGAGGCTTACCACGAATAAGGATGAGTGTGAGATATCAACTTCTCAGTACT
TGATGCAACTCAACCAATTTCGGGGCGGACATCAACTGACCTGTCTCAGTACCTGTGTCTT
CCCTGGGTCTCGAGGACTACGTGTGCCCAACCTGGACCTCAGCAACCCAGGCGTGTCCG
GGACCTGTCTAAGCCCATCGGTGTGGTGTGAAGCCCAAGCATGCCAGCTCTGTGAGGGAGAAT
ATGAAGAAGTTTGAAGCCACGAGGAGCAATTGACAAGTTCCACTATGGCACCACATCTCC
AATGACGAGGCGTGTATGCACTACCTCATCGCTGGAGCCCTTCACTCTCTCGACGTCCA
GCTGCAAAAGTGGCGGCTTTGACTGTCTCGCAGCGGCACTTCCACTCGGTGGCGGACGCTGG
AGGCACCGCTGGAGAGCCTCGCATGTGTGAAGGAGCTCATCCGGAATTTCTTCACTTCTCT
GACTTCTGTGAAGACCAAGAACGTTTGTAGCTTGGCTGTCTCCAGCTGACCAACAGAGAAGT
AGGCTGTGTGGTGTCACTCCCGCTGGGCGAGCTCTCTGAGGACTTCATCAGCAGCAGACCG
AGGCTCTGGAGTCCGAGTATGTGTCTGCACACTACAGCAGTGTGATGCACTCATCTTGG
TACAAGCAGCGGGGGCGAGCGCGGAGAGGCCCTCAATGTCTTATTAFTGACACCTATGAG
GGGGGCTGTAGACTGTGACACTTGACATGTGACAGATGAGCGGAAGCGGAAGGCTCTGGAGGGCAAT
TCAAGCAACTTTGGGCAACTCTCTGTGACGTGTGTGAAGGAGCCACTTCACTCTCGGCTCA
CCTGAGGAAGCAGGCGCACTCGCTTGCACGCTGGACACTTAATCACTCAGTATGATCTTCCAGCA
CTTGACGCAACTCAAGGCATTTCTTGCAGCAGGTTGACTGTGAGTGCCAGTGGGCTGTGGGCA
CCCCAGCACTGGTGTGCCATGATGCCCAACATAAGCAACTTGTGACCTTCAAGTCTCAGCAAGAACCC
ACCATGGGCGACCAAGCAGCAGCACTGTGAGTGGCCCGTGGGTGCGAGCAAGTGGTGT
GAGTGTGAACAAGCATTGGCAGTGGCGCCCGGATGGAAGAATGCTGATTCAGCGGTGGCCACTGG
ATGGCAGCTCTCGGGGTGACTGCATCACTCCCGTGGCAAGCTTTGAGCAGCTCAGCTGCCAC
CTTGATGTATGAATCTGCTTGCAGCTGACGAGCACTGTGGGACTTACCTCATCTCAGGCTCCG
GGACCAACCGTGCATGTTGTGGCGGCTCTTGATCATAGGCTGGTCTGTGACTAGGCTCTGGCA
CAAAGCTGTGACAGCTCTGTATGGGCAATGGGCTCAGTGAGCTGTGTGGCCATCAGCATCT
GAACTTGACATGGCTGTGTCTTGATCTGAGAGTGAACATGTGATCATACACTATGACCGC
CGGACAGTTTGTAGCGGCATCAAGGCTCTGGGTGGCCATTTCCCTGGACCTATTTTCCAC
TGGCACTTGGGTTCCGAAGCGAGATTGTGGTACAAGCTCAGCTGGGAAGCTCTGGGGCG
CAGGTCACTTACTCTTGCATCTGTATTCACTGATCAATGGGAAGTTTGGGGGCTTCACTGCCCC
GGCAGAGCAGCTCAGGCCCTGACGGCTGACGAGTGTGACAGGAGCTTTGTGTTGTGGGACGCCG
CGCCGCTGCACATCTCCAACATAAACCACTGTCTCCCGCGCGGCTCTCCCTTGGCCATGAG
GTGGCCATCCGCAAGGTTGGCGGTGACCAAGGAGCGCAGCCACTGCTGTGTGGCGCTGGAGA
TGGCAAGCTCATCTGTTGGTGTGGCGGGGACCGCTTGAGTGTGGCAGCAGCCAGCTTCCGCG
GGAAGCTGTGGCGGTCTCTCGCGCGCATCTCCAGGCTCTCCGGGAGCAGGGAATCAAC
CCTACTGAGGCGCGCCTGAAGCTTGGCAGCTCGCGGCTCTCGGGCGCCGCGCCGCGGAGCTGT
GCCCGGAGCCGCCCGCCAGAAGTTCGCGGGGAACACCCCGGGGTGGGCAGCCAGGGGGTGT
GCGGGGCCCCACCTTCCCGAGCTCAGGGAATGGCGGGCGATGTTACCCCTCAGGGAATGGCG
GGCGAAGTCCCGCCCCCTCGCGGCTGAGGGCGCGCCCTGAGGCGCAGCACTGGCGGTCT

FIGURE 23

MSQFEMDITYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRKLKLPVN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELAELETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPOEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPITLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFKH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSDRQFHSVAAAWQARLESFADVKELIP
 EFFYFPDFLENQNGFDLGLCLTNEKVGDVVLPWPASSPEDFIQQHRALESEYVSAHLHEW
 IDLIFGYKQRGPAAEEALNVFYCYEGAVDLHDVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSGPPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLHLQGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFPGPIFHLLALGSEGQIVVQSSA
 WERPGAQVTSYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTCGTGGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAACTATGGGGTCCGGGGCTCTTC
 TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
 ATAGCCCGGTCATCTTGGAGTATATTGACCAACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTTCACTGCTACTCATGCGAAACATTGTCAGGGTGGTGTCTCTGGACAAAGTCACAGA
 CCTGTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCTGGGGGCCTATGTATCGCCAGCGGCTTCTTCAGCGT
 TTTCCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTTGAAGACCTGGAGCGGAACAACG
 GCTCCTTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTTAATC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLQIYGVLG
LFWTLNWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALITL
VQIARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKN
FCVSAKNAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFK
SPHLNYYWLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSK
SLLKILGKKNEAPPDNKKRKK

100
90
80
70
60
50
40
30
20
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**TTTCGTGTCGGAATTTCCGCAAAGAGTTCTACAGGTTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAGATCCTTCAGGCTTGTTC
 CAGTGTGACCACTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTTGAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTGAAGGAGAATTGCGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAAGTT
 TCTGGGCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTGCACAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCCTTTGTGTGTCGACAAAGAACCAGGCGCTGCAAACTGCTGCCCCGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACACAGCTCCCGGA
 TGCTGCAACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCT**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCAATTTAGATTGAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGSEFSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFLADMGPLPKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSRNLKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQEPGQGSKGDKGEMGSPGAPCQKRK
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENATYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

[illegible]

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPDPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLSDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGVPVQPDQCPSTCLNGGTCHLGTTRHHLACLCPE
GFTGLYCESQMGQTRFSPPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGS SVQLRSLRL
TYRNLSPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSP LHAKEYI

FIGURE 33

GAATCATCCACGACCTGCAGCTCTGCTGAGAGAGTGCAGCCGTGGGGGTTTGTAGCTCAT
 CTTTCATCTATCATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACAAATGAGACTCATCAG
 AAACATTTTACATATTTTGTAGATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGAATGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTCCCGCAGAGCTTG
 ACCCAGCCACCAACGACCTGGATTATCCTATAACCTCCTTTTCACTCCAGAGTTTCAAG
 TTTTCTATCTGTCTCCAACTGAGAGTTTGTATTCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGCTCAGGTATTTAGATCTTTCTTTTAAATGACTT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTCAACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCAGAAAATTGCTCATCTGCATCAAAATCTGTCT
 TTTCTAGGATTGAGAACTTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
 AAAATGCAATGTTGTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAATATTAGAAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTCTTATTGCTTAAATAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTGGCATAACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAAACTGTAAATGAGAACTATAAAATGGAGCATGTACATTTCCAGAGTGTTTTACATTAC
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATGAGAAACCTGACAAATATCAAAATG
 CACAAATGCGCACACATGCTTTTCCGAATTTCTCTACGAAATTTCAATATTTAAATTTTGGCC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAATCTTCAACTGCCCTCATTGAAAACCTCT
 CATTTTGAATGGCAATTAACCTGGAGACACTTTCTTTAGTAGTTGCTTTTGCCTAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATATGATGAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCTACATAAAATTTGTGATTTCTGTCTCAG
 GTGCTTGGCCAAAAGTATTCAAATCTTGACCTAAATAATGACAAATCCAACTGTACCTA
 AAGAGACTATTTCATCTGATGGCCTTACGAGAACTAAATATGCAATTTTAAATTTTCTAAATG
 CTCCTTGGATGCACTTTCAGTAGACTTTTCTGATTTCTGAACTTGAATGAACTTCATTTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCCGGGAAGAA
 ATCCATTCGGGTGTACTGTGAATTAAGAAATTTCTTTCAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTTCATACACCTGTGAATACCCCTTTAAACCTAAGGGGAACATG
 GTTAAAGACGTTTCATCTCCACGAATATCTTGCAACACAGCTCTGTTGATTTGTCACCATTTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAAACCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCATTTATTTATACAGTGAACATGATTTCTC
 TGTGGGTGAAGAAATGAATGATCCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGATTGCG
 CTTTATGAAAGCTACTTTGACCCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTGCCAGATGAGTGGTGCCATT
 ATGAATCTCACTTTGGCCACCACAATCTCTTCCATGAAAATTTCTGATCATATAATTTCTATC
 TTACTGGAACCCATTCATCTATTGCAATCCCAACAGGATATCATAACTGAAAGCTCTCTCT
 GGAAAAAAGACATCTTGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCCAA
 ACCCTCTGAGCTGCTATTAATGTTAATGTATTAGCCACAGAGAAATGTATGAATGCGACACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAAATGTGGCCAGTTGCT
 ATAAATCCCAAGCTCCTTGGGAAGTTGGGGACCATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAAGTGGTTATCTGCTCATATA
 TCAGTTTCTAGAAGGATTTCTAAGAAATGTATCTTATAGAAACACCTTTACAAAGTTTATAGG
 GCTTATGGAAGAAGGTGTTCTACCCAGGATTGTTATAGATCAAGAAAATGTGGCCAGGTTGCG
 AGTGGCTCACTCTTGTAAATCCCAACACTATGGGAGGCCAAGGTGGGTGACCCACAGAGGTCGA
 GAGATGGAGACCATCTGGCCAAACATGGTGAACCCCTGTCTCTATAAAAATGCAAAAAATTA
 GCTGGGGCTGATGGTGCACGCTGTAGTCCCAGCTCACTTGGGAGGCTGAGGCAGGAGAAATCG
 CTGGAACCCGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCTGGT
 GACAGGCGGAGCTCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGTGAACAAACATCC
 TCATGGCCACAAAATAAGGTTCAATTCATAAATATAGTACATTAATGTAATATAATATATA
 CATGCCACTAAAGGAATAAGGTAGCTGATATTTTCTGGTATGGAAAAACATATTAATAT
 GTTTATAAATCTATTGGTTGGTGCAAAACATAATTTGCTGTTTGGCAATGAAATGGCATTGGA
 ATAAAGGTTAAGAAATCTATACAGAGTGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA
 TTAGGAGGAGCATTTGATTTCATATGTTGTGATTTTCTATAATGTTTGAATGTTTGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAGATAGTTTTTACAGCT

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FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENCSPETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENDHIIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCTCGGAGGGGTGCGCGGGAAGG
 GAGGGAAGAAGGAAGCGGGGCGGGCCCTGCGCCGCGCCCGCGCTTGTGCGCGCCCTGTCCGCGCCGGC
 CCAGCCAGCCGACGCCCGCGGGCGGTACACGCGCAGCCAGCGCGCCCTCCGCGGCCAAGCGCGCGT
 CTGCTGTGCTGCTGCCCTTGGCCCGCGCAGCTTCTGCGCCGCGAGCCCGCGCGCCCGGTGAGCGTGA
 CTTGCTGCCCTGGGCGCGGGCGGAGGCAATGTCGCCCGGGGACCGCTACCCAGCGCTGGCCCTGTGGTCT
 CTGGCAGTGACCTGGCCGGGTGCGAGCCAGGCGCAGCCCTCGAGGACCTGATTATTACGGGCGAGGAGAT
 CTGGAGCCGGGAGCGCTTACTAGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCTCCGCGGGC
 CCGGGGAGGAGTGGGAGCGGCCCGCCGAGGAGCCAGGCGCCCGCAGAGGGCCACCAAGCCACAAGCTCCC
 AAGAGGGAGAAGTCCGCTCCGGAGCGCCCTCCACAGGTAAACACAGCAACAAAAGTTATGAGAACCAAGAG
 CTCTGAGAGGCTGCCAAGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCCTCCACGGTGAAGCGCTATGGCTGGGGCA
 CATCGAGGGAGACTCAACATCCAGCGGGCATTAAATGAAATGATTTTATGACGGAGCGTGGTGGCGGGGAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACCAGATTCACTGGTGTCACTCAAGGGA
 GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACAGCTGGTC
 ACTGTTAAGAATGGATCTGGAGACATGATATTGAGGGAACAGTGAGAAGGAGATCCCTGTCTCAATGAGCT
 ACCCGTCCCATGGTGGCCCGCTACATCCGCATAAACCTCAGTCTGTTTATAATGGGAGCATCTGCATGA
 GATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATATCACCGCCGGAAGAGATGACACCACCT
 GTGACCTGGATTATAAGCACCAATATAAGGAAATGCGCCAGTTGATGAAAGTTGTAATGAAATGTGTCC
 CAATATCCACAGAATTACAACTATGGAAAAAGCCACAGGGCTGAAGCTGTATGCTGTGAGATCTCAGATC
 ACCCTGGGAGCATGAAGTCCGTGAGCCGAGTTCACACTACATCCGCGGGGCCACAGCAATGAGGTGCTGGGC
 CGGAGCTGCTGCTGCTGCTGGTGAGTGTGCTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATGCTCCACCT
 GTGGAGGAGACCGGATTACGTCCTCCCTCCCTCAACCCGAGTGGCTGCGAGAGGCCCTACGAGGGGGCT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATGACATCAACAACAATTTCTCTGATTATA
 AACACGCTGCTCTGGGAGGCAGAGGATCGACAGAATGTCCCGAGGAAAGTTCCCAATCACTATATTGCAATCCC
 TGAGTGGTTCTGTGCGAANAATGCCACGGTGGCTGCCGAGACAGAGCAGTCATAGCTGGATGGAAAAATCCC
 CTTTTGTGCTGGCGGCCAACCTGCAAGGCGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGCGTCCCC
 TGGAGACCGCAGGPACACACCCCCACCCCGATGACCAGTGTTCGCTGGCTGGCTACTCCTATGCCTCCAC
 ATCGCCCTCATGACACAGCCCGCGAGGAGGTGTGCCACACGCGAGGACTTCCAGAGGAGGAGGCACTGTCA
 ATGGGGCTCTCTGCGACACCGCTCGTGGAGTGTGAACGATTTCACTACCTCATACAACCTGCTTCGAAGT
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGGAATAACCGGGAATC
 TCTGATCTGTTCTGAGGACAGGTTTATCGTGGCATTAAGGCTTGGTGAGAGATTCAATGGAAAAAGGAATCC
 CAACCGCATTTATCTCCGTAGAAGGCATTAAACATGACATCCGAACAGCCAACTGGGATTTACTGGCGCTC
 CTGAACCTTGAGAGTATGTGGTGACAGCAAGGCCGAAGTTTCACTGCATCCACAAGAATTCTATGGTTGG
 CATGACATGGGCGCACAGGTGTGACTTACACATAGCAAAACCAACATGGCGAGGATCGAGAGATCATGG
 AGAAGTTTGGGAAGCAGCCCTGACGCTGCCAGCCAGCGGCTGAAGCTCGGGGGCGGAGAGACGACAGGCT
 GGGTGAACCTCTGGGCGCTTGAGACTCGTCTCGGACCCATGCAAAATTAACACACTGGTAGCTCATAG
 TGGACTCACTCACTGTTGTTTCTCTCTGTAATTCAAGAAGTGCTGGAAGAGAGGTCATTTGTGAGCGAGTCC
 CAAAGGGAGAAGCTGAGGCTGAGGCTGTTTCTTTCTTTGTTCCCATTTATCCAAATTAATCTGGACAGCA
 CGAGAGAAAAGCTGATGGGAGTGAGAGAATCAAGCAAGCCAACTCGGGAATCAGAGAGGAGGAGGAGGG
 GAGCCTGTGCGTTGAGAGCTCTGGCTGCATAGAAAAGGATTTCTGTGCTTCCCTGTTTGTGCTGGCAGCAAG
 GTTCCAGCTGCAATTTGCAATTTGCGACGTAAAATTGCGAGCATTTCCCGAGCTGGGTCTGCCAAATGTATCA
 ATTTAGATGCTCCAGCGCTCTAGAGAAATCCACCTCTCTGGCCCTGGGACATTTGCAAGCTGCTCAAAATTA
 TTTCTGTGTTCTTTGACAAATGCTCATTTGCCAAGTGACATCAGTAGGCTCTTGAATCTGTTTACTCTCTCT
 TTTTCAACAAGGAGTGTGTTTCAGAAAAGGAGAGAGGCTGAGATCATTCAGAGATTGTTGGGCGCAGAGCA
 TGGAGCTTACCTGCAAAATTTGAGGCTCCATAAACACCCCAAGTCCCTGCTGATCCAGTAGCCTGGAGTT
 CCCAGGTTAGGAGAGCGAGGAGTCCAGCCTTCTGAAAGGCCAGAAAAATTAGCCTGGATCTCTCTTTTAC
 CTCTAGGACTGGAAGAGGACGAGTGGGTGGCTCTCTGCTTGAAGTATTGCCCTGTGTG
 GAATTGAGTGTCTATGGTTGACCTCATCAGCCTGGGAGTATTTTTGTGTAAGATGCCAGATCTTCCA
 GATTAGGCTAAATGTAATGAACCTCTTAGGATTACTGTGGAGCATGATTGGAGGAATTTGAATTTAT
 CTTGCAAGAAAAAGTATGCTCACTTTTGTGTAATGTTGCTGCCTCATGACCTGGGAAAAATGAAAAAAA
 AATAAGCAATGTGAAGCCTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPHYARPEPELETFSPLP
AGPGEWEERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVNVEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFDPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQP VSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCGGCCTCTCATTTCCTAGCCCTCTGTCTCTCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTTGACTCCAGCTCCAGC
 TGCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT
 TTCCTAATTCCACGGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTTCCTCCGCGGACACACCTTTTC
 CCGTGGACAGAGTGGAAACGCTTGGAAATCACAGCTCATGTTCTTCTCAGAAATTTGAGAAAGAACTTCTAAA
 GTGAGGGAAATATGTCCAATTAATTAGTGTGTATGAAAGAAACTGTTAAACCTTAACCTGTCCGAATTGACATCAT
 GGAAGAGGATACCAATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTGAGAACTGAAGGAGATGGAAGAAAC
 TGGTCTATACAGCTGAAGGAGAGTTTGGTGGAACTCAGAAATTTGTGACCAGCTGGAGCTGGAGATAGAATAT
 ATGACTCTCTTGGTAGAGAGCTTGAGACACTAGACAAAACCAATGTCCTTGCCATTGCCCGAAATCCTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAAGATCAAAACACCCCTGTGCTCCACCTCTCCCACTC
 CAGGGAGCTGTGGTCAATGTGGTGTGGTGAACATCAGCAAAACCGCTGTGGTTTCAGCTCAACTGGAGAGSGTT
 TCTTATCTATATGGTCTTGGGGTAGGGATTACTCTCCACAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAAACACACTGGAGTATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAAGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTATTATCACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTCT
 GTATGCCACCCGCTACTATGAACACCAGAACAGAGAGATTTTTTACTATTATGACACAAACACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTTAACTATAACCCCTTTGACCAGAAA
 CTTTATGCTCTATAACGATGGTACCTTCTGAATTATGATCTTCTGTCTTGCAGAAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAGAAAATGTTTGTGAAAAATAGTCTTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAGTGTGTCATTTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGTGGAGTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAAGTCTGTCTAGGGTGGGA
 TTGTCAGAGGCTCAGGGGCACTGTGGGCCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTTAAACCTCAGATGGCGCTCAGGGATTCTTTGACAGGAAATATTGCCCAATGACTAGTCT
 CTCATCCATGTAGCACCACTAATTTCTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGCTAGATTATATCT
 GGAGCTCTCGAGGGACCAAATCTCCAACCTTTTTTCCCTCACTAGGACCTGGAATGATGCTTTGTATGTGG
 CAGATAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGGTGCTGAGTTTATGGAGAGAGGCCCTTTT
 ATGCATTAATTTGTACATGGCAAATAAATCCAGAAGSATCTAGATGAGGCACCTGCTTTTTTCTTTCTCTC
 ATTGCTCCACCTTACTAAAGTCAGTAGAATCTTCTACCTCATAACTCCTTCAAAGGCAGCTCAGAAGATTAG
 AACAGACCTACTAAACCAATTCACCCCCACCAACCCCTTCTACTGCCACTTTAAAAAAATTAATAGTTTT
 CTATGSACTGATCAAGATTAGAAAAATTAATTTCTTTAATTTTATTATGGACTTTTATTACATGACTCTA
 AGACTATAGAAAAATCTATGCGAGTGACAAAGCTGCTAGCATTTATGTTATCTAATAAAGACCTTGGAGCATA
 TGTGCAACTTTATGAGTCTATCAGTTGTGTCATCTAATTTTGCCCTTTGTTTAAGCCTGGAACCTGTGAAGAAAT
 GAAATTTAATTTTTTTCTAGGACGAGCTATGAAAAAGCTATTGAGAGTACTAGTATTAATCAGTGCAGTAGT
 TGGAAACCTTGCTGGTGTATGTGATGCTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGCTATTTTT
 TCCCTTTGATGTTTCAGTCTCTAGTCTATAGGATTGGCAGTTTAATGCTTTTACTCCCCCTTTAAAAATAATGAT
 TAAAAATGTCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLALLFFFLGQAAGDLGDVGPPIPSPGFSFPGVDSSSSSFSSSSSRGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPQHHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYQGSGTAVYNNNMVNMVNTGNIARVNLTNTIAVTQTLFNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVLYATRTMNTREEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG
YLLNYDLSVLQKPQ



FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTTGTGGAGATGGGGGAGCGTCCTGGGGGTGTGCTCCATGGCGAGCT
 GGTATACCATTGTTGTGTGGAGTCCCCGCTGTTTGCATGCCGATGCTGTCTCATGTGGAAC
 AACTCCACTCTTAATAGATTGATCTATGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTG
 TGTAAATGTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTCGATTGTTGTGAGAACT
 AGAAGGGTGTGTCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTGTGGCTATGTTCTATCTTCTTCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGAATTA
 TTATTGGGCAATTTCTTATCCAGAAGGAACTTTACAACCTGTGTGGTTTTATGTAGGCATG
 GCAGTGGCTTTGTTTCATCCTCATACAACTAGTCTTACTTATTGATTTTGCACATTATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCCGCTTGT
 TATCAGCTACAGCTCTGAATTTATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 CAGTCTATCCAGCCAGTTGTTACAGAAAACAAGGCGTTTCATCAGTGTCAACATGCTCCTCTG
 GCTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAAACCAAGATCTGGTT
 TGTACAGTCTTCAGTAAATTACAGTCTACACAATGATTTGACATGGTCAGCTATGACCAAT
 GAACCAAGAAACAAATTCGAACCCAAAGTCTACTAAGCATAAATTGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGGTGCCATGCTCAAGGAATTATAGGACTAATTCT
 TCTTTTGTGTGTGATTTTATCCAGCATCCGTAAGTCTCAAAGGATGCTCAGGTTAATAAAA
 CTGACTCTGAACAGTGAATCTACATTAATAAGAAGTGTGAGGACTAGAAGTGAATGATC
 ACTGGAGGATGGGGACGATGTTCCAGGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GATTTCTTCTTCTTCACTTCAATGCTTTTCCCTGGCTTCACTTTATATCATGATGACCTTACC
 AATGGTCCAGGATGAACCCCTCTCGTGAGATGAAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACACTCGTGGCCACCACTGGTTC
 TTACAAATCGTGATTTTGACCTGAGTGAAGTCTTAGCATGAAAGTCCCACTTTTGATTTATGTC
 TTTATGAAAACAGTATTTCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTCTTACCAG
 TGGCATTGATATGTGAAGTGAATGAATTGCAGAGGAAAGTTTTATGAATTTGGTGTAGAT
 TAGTAAAAAGTGGCCATTTATGGGCTTATTTCTCTGCTCTATAGTTGTGAATGAAGAGTAAAA
 CCAAATTTGTTTGACTATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATAAAA
 CCAAATGTAATGGTGCCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATCTGCAAGAAC
 ATGGTTTTATTTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTATACCTTGATACGGAAATTTACACAGGTAGGGAGTGTTTAGTGGACAAATGTGTAGG
 TTATGGATGGAGTGTGCGTACTAAATGAATAACGAGTAAATATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTTTTGGTTGTTTTAAACTCATGAAGTATGGGTTCACT
 GGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATTAATCATGGGTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCCAGCACGGTAGCTCACCCTT
 GGTAAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGGCCAGGAATTCAGACCA
 GCTTGGCAGATGTTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCCTTGGTCT
 CAGCATGTGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGTTGCAGTGAGTGAAGTCA
 CGTCACTGCATCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATGAAATCAAGG
 AGGCAAAATTTTGACAGGGAAGGAAGTAACCTGCAAAACCACTAGGCTTTAGTAGGTAAT
 ATAAATCTAGTCAGTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 CTGAGATGACTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATCTCTCTGACATTTAA
 AAATATTTCTAATCAAATACATGATATTGATTTACACCTCATACTGTGATAAATTAAGT
 GATGTGAATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAGAAATGATGAATGTTTT
 AGAATAAATCCTGCTTATAGTATACACAGTCTCAAAGATGTTTAAATGCTTTTGTAT
 TTTACTGCCATGTAAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTAGTTATTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAAAT
 TCTTCTTTAAAAATATTTAATGTGAATGGAATATAACAAATCAGCTTAAATTTCCCAACC
 TTATTTCTGTGTAGACATTTGATTTCCAAATTTTGAATGGCTGTGTTTTACCTCTAAATTA
 ATGAATTCAGAGAAAAAAGAAAAA

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FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTYSSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAGTAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTTGCTTGTTGGAGTANGTGAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAATGGATTTTGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

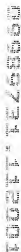


FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACATCATCCAGCCAGTTGTTCAGAAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTTGCATTGAGCTGCGGGTTCGCGGCGCGCGCGGCTCTCCAAT
 GGC AATATGTGTGGCTGGAGGCGAGCGGAGGCTTTCGGCAAAAGGCAGTCAGATGTTTGCAGACC GGGGCGAG
 TCCTTGTGAAAGCAGATATAAAGAAACATTTATTAACGTGTCAATTACGAGGGAGCGCCGCGCGGGCTGTGCG
 ACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGAGAAGAAGAACGGGAAAAGAGGCAGATTCAC
 GTCTGTTCCAGCCAGTGGACTCATGATGGCCCTCTCGTAATTTATCAGATATTTGATTTATTAAGCATGCC
 CCTCGTTTGTGTGTACGCACACACAGTGCACACAAGGCTCTGGCTCGCTCCCTCCCTGTTTCCAGCTCC
 TGGGCGAATCCACATCTGTTTCAACTCTCCCGGAGGSCGAGCAGAGCGAGTGTGTCGAATCTGCGATGT
 AAGAGGGACGAGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACCCAGAT
 CAGCAAAAAAAGAAAGATGGGCCCCCCGAGGCTCTGCTGTGCTTGTCTGTCGCCAACTGTGTTCTCCCTGCTGGG
 TGGAGCTCGGCTCTCTGTGCGACACCGCTTGAAGGCGAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA
 ACATCATCTCGTGTGACGAGACGACCGAGTGTGAGCTGGGTTCATGCAGGTGATGAACAAGACCGCGCGC
 ATCATGGAGCAGGGCGGGGCGCATTTATCAACGCTTCTGTACCACACCCATGTGCTGCCCTCAGCTCCTC
 CATCCTCACTGGCAAGTACGTCCACAACCAACACACTACACCAACAATGAGAAGTGTCTCCGCTCTGCTG
 AGGCACAGCAGAGAGCCGCACCTTTGGCTGTACTCTAATAGCACTGGCTACCGGACAGCTTCTTTCGGGAAG
 TATCTTAATGAATACAACGGCTCTACGTGCCACCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAAATCTCCG
 CTTTTATAACTACACGCTGTGTGCGAACGGGTGAAAGAGAAGCAGCGCTCCGACTACTCCAAGGATTAACCTCA
 CAGACCTCATCAACCAATGACAGCGTGAAGTCTTTCGCGACGTCCAAAGAGATGATCCCGCAGACGGCCATCTC
 ATGGCTCATCAGCCATCGAGCCGCCACGCGCTGAGGATTACGCCCAACAATATTACGCTCTTTCGCAACGCG
 ATCTCAGCATACAGCCGAGCATCAACTACGCGCCCAACCCGGAACAAACATGGATCATGCGCTACACGGGGC
 CCATGAAGCCCATCCACATGGAATTTACCAACATGCTCAGCGGAAAGCGCTTGCAGACCTCATGTGCGTGGAC
 GACTCCATGGAGACGATTTACAAACATGCTGTTGAGACGGGCGAGCTGGACAACAGTACATGATATACACGCG
 CCGATGAAGCCCATCCACATCGGCCAGTTTGGCTTGGTGAAGGGAAATCCATGCCATATGAGTTTGCATCAGGG
 TCCGCTTCTACGTGAGGGGCCCAACGTTGGAAGCGGCTGTCTGAATCCCAACGCTGCTCTCAACATTAAGCTG
 GCCCCACCATCTGTGACATTTGAGGCTGGACATACCTGCGGATATGGACGGGAATCCATCTCAAGCTGCT
 GGACAGCGAGCGGCGGTGAATCGGTTTCACTTGAAGAAGAAGATGAGGCTGTGGCGGAGCTCCTTCTTGGTGG
 AGAGAGGCAAGCTGCTACACAAGAGACAAATGACAAGGTGGAGCGCCAGGAGGAGAATTTCTGCCCAAGTAC
 CAGCGTGTGAAGGACCTGTGTGAGGCTGTGAGTACCAGAGCGGCTGTGAGCAGCTGGGACAGAAGTGGCAGTG
 TGTGAGGACCGCCAGGGGAGCTGAAGCTGCATAAGTGCAGGGGCCATGCGGCTGGCGGCGAGCAGAGGCC
 TCTCCAACTCTGTCGCCAAGTACTACGGGCGAGGCGAGGCGCTGCACCTGTGACAGCGGGGACTACAAGCTC
 AGCCTGGCCGCGACCGCGGAAAAAATCTTCAAGAAGAAGTACAAGGCCAGTATGTTCGCGAGTGTGCTCCATCCG
 CTCAAGTGGCCATCGAGCTGGACGCGCAGGCTGTACCAGCTAGGCGTGGGTGATGCCCCAGCCCGGAAACCTCA
 CCAAGCGGCATGCGCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTCTAGTGGCACTGGAGGCG
 CTTCCGACTACTCAGCCGCCAACCCATTAAGTGAACATCGGTGCTACATCTGAGCAACGACACAGTCCA
 CTGTGACCTGGACCTGTACAAGTCCCTCAGGCTTGAAGAAGCACAAGCTGCACATGACACAGAGATGAA
 CCGTGCAGARCAAAATTAAGACCTGAGGGAAGTCCGAGGTACCTGAAGAAAGAGCGGCAAGAAGATGTGAC
 GTGCACAAAATCAGCTACCAACCCACGACACAAGAGCGCGCTCAAGCACAAGGCTCCGCTGTGCTCCTTTAG
 GAGGGCTCGAAGAGAGAGGACAAAGTGTGGCTGTGCGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTCG
 TCAAGCGCTCGCAAGAACAGCAGCGTGCAGCATGCCAGGCTCACTGCTTCCACACACAACAGCAGCTGG
 CAGAGCGGCTTCTTGGACATCGGGGCTTTCTGTGCTGCACGCGGCAACAATAACAGTACTGTGTGAT
 GAGGACCATCAATGAGACTACAATTTCCCTCTTGTGATTTGCAACTGCTGCTTCTAGAGTATTTGATCTCA
 ACACAGACCCCTACCGACTGATGAATGCAGTGAACAGGAGTGTCTCCACAGCTACACGTACAGTACAG
 CTCATGGAGCTGAGGAGCTGCAAGGTTTACAAGCAGTGAACCCCGGACTCGAAAGACTGGACCTGGATGGAGG
 AAGCTATTGAGCAATGACAGGCAATTTACGCTCGAAAGTGGGCGAGAATGAAGAGACCTCTTCCAAATCTGG
 GACAACCTGTGGGAAGGCTGGGAAGGTGAAGAACAACAGAGGTGGACCTCAAAAAGATCAGAGGCTCAGACTGA
 CAGCAGGCAATGAAAACCATGTGGGTGATTTCCAGCAGCAATGTGCTATTGGCCAGGAGGCTCAGAAAGG
 AAGCAGCACTCTCAGTCAACATGCAGATTTCTGGAGGATAACGAGCAGGAGAGATTAACCTCAGGAAGTCC
 ATTTTGGCTGCTTTGCTTTGGATTATACCTCAGCAGTGCACAAAATGCAATTTTTCGTATCAAAAAGTCA
 ACCATAACCTTCCCGCAGAGACTCACAAGGAAAAGCGGAGAGAGCGAGCAGAGAGATTTCTTGGAAATTTT
 CCAAAAGGGCGAAAGCTATTGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCCTCTATTCTT
 TGGTTGTGCACAAAGAGGAAGTAAAGAGCAGGACAGAGGCAACGTGGAGAGCTGAAAACAGTGCAGAGAG
 TTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTTACAGCAATAAAACCTCGGTGCTGCTGAGAGAA
 CTGCTTCTATGTATATGTGACTATTTACATGTAAATCAACATGGGAATTTTAGGGGAACCTAATAAGAAAT
 CCAATTTTCAGGAGTGGTGGTCTCAATAAACGCTCTGTGGCAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
SYNYAPNPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPFYVRGPNVEAGCLNPHIVLNIIDLAPTILDI
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDL CQRAEYQTACEQLGQKWQCVEDATGKLKHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYIILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKREECDCHKISYHTQHKGRCLKHRGSSL
HPFRKGLQEKDVKVLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFACTSANNNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCCCCACGCCACCATCCCCGCCA
CGCTCGCTGAGGCTGCTGTGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGAAGTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNVRRRAQPWPFR
RRHGLGIFHHHRHPGHVSHVFNVLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCGTAAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTTGGGGCAGCAGCCGTGGCTGGGAT
 GACGTTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGCACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGTC
 TCCAGGCCCTTGTGAAGCCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATR RVHPALD TYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAA TLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
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FIGURE 52

CCGCGGGAAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTC**ATG**ACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCCTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCTCATTGGGTATCACCTATACAGAAAGCCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGTTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTCTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGCTAAAAATCGGGGGAG
 TGAGCGGGCCGGCGCGCGCGACACGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCTTGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAGAAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACCAAAAAATCTATTGTGGTATGCATTGATTAACCTT
 ATAAAAATGTTAGAGGAAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCGGTGG
 TCAAAATTCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAAT
 GTAACTGGCTTTTGAGGGTCTCCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCAGCCACCAGGCTCCCTGTGTCCCTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
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DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG



FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGCGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT



GGGAGGCTGTGNCGGCTTTTGTTTTNTTGGCTAAATCGGGGGAGTGAGCGGCCCGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGCGGGTGGACTGACCTGAAAAAATGTTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAGCGCAATACATATT
GCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTGTCTGGGTCAAAACAGGTGCTCGCATTTGGCTTTTCCTGGTGTTCATGTTGGCCCTTTGG
ATNCTGATTCGATCTATGTGGATCTTTTTGGAGGTTATGTTGCTCAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTAATTTTTCAGAAATGCCTCATNTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCGCTGGTGCTGCTCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGGCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGTTCTCAAACAAGC
TTTTTCAGGCTGACAGTCAAAATTTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGCTGGAACAACAT
GCTCGGCTGCAAGTCAAGTCCCTCTGCTCTCTCTTTGACATCATGGTACTGGAAGGGCCC
ACCAGGGCAGGGGGCTGCTGTCATACCTTTGGAAGAATGGCCTTGAAATTTGACACAGGAAT
CCATTAGATTGGGGCTGATGGAAGAGGGCAGCATTGGCCCTTTTATCTTTGGACAGATCACTG
AAGGGCAGCTGGACTGGCTCCCTCTGCTCTCTCTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
CTTGAGGCCCTCATGCCATCTCTTTGAAATTCCTCCCATTTGCCGTGGTTAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTCTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTCTCAGCAGCTGGGGGGCTCTCTGAGCTCCAGGCAGTACTAGCTACATCTTCCCCA
CTTAGCGGTGTCACCCCAACACAGTGGCTTTCCATGCACGGCCTGCTGGTCAACCACATC
ATGAAGAGAGGCTTTTATCCCCGAGGGGGTTCCAGTGAATTCGCTTCCACACCATCCTGT
GATTACGGGGCTGGGGGCGCTGTCTTCCAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCTGTGGTGTGCTAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATCTGTGGTCTCCAGCAGCAGTGTCTCAACACCTATGAACACCTACTCGCCGGGGAACGC
CCGCTGCTTGCACGGTGTGAAGCAGCAACTGGGGACGGTGGCCCGGCTTAGGCATGACCT
CTGTTTCTCATCTGGCTGCGAGCACAAGGAAGACCTGCATCTGCCCTCCACCAACTAGCT
GTTTACTATGACACGGCATGGACACGGCGATGGAGCGTACGTCCTCATGCCCCAGGGAAGA
GGTGGCGGAACACATCCTCTTCTTCTTCTGCTTTCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGCGGCTCCACCATGATCATGGCTCATACCCACTGCTACGAGTGGTTT
GAGGAGTGGCAGCGGAGCTGAAGGGAAAGCGGGCAGTGACTATGAGACCTTCAAAACTC
CTTTGTGGAGGCTCTATGTCAAGTGGTCTTGAACCTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTCACTCAGGATCCCCACTCACCACACAGTTCATCTGGCTGCTCCCCGAGGTGGC
TGCTACGGGGCTGACCATGACCTGGGCGCCTGCAACCCTGTGTGATGGCCTCCTTGAGGGC
CCAGAGGCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTCAGCTGTGGACTGGTCTG
GGGCGCTGCAAGGTGCCCTGCTGTGACGACGCGCATCTGAAGCGGAAGTGTGACTCAGAG
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAGAAAT**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCACGTATAAAGCACTCTAATTTGGTTCTGATGCCCTGAAGAGAGGCCTAG
TTTTAAATCACAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGCGAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGTGAT
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCATTGCTCTTCACTGATGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTGAGCTCAACCTGGTGGGTTCAGTTC
TGTCTGAGGCTTCTGCTCTATTCAATTAGTGTACGCTGACAGTCTACACTGTCAAGG
GAAAGGGAGACTAATGAGGCTTAACTCAAACCTGGGCGTGGTTTTGTTTGGCCATTCCATA
GTTTGGAGGCTCTAGATCTCTTTTGTGCTGGGTTCAGTGGCTCTTCAGGGGACAGGAAT
GCCCTGTGTCTGGCCAGTGTGGTTCTGAGCTTTGGGGTAAACAGGAGATCATCAGTTAGTA
GGGTGACGTGTGATGATCATATCCAATTATATGGAAGTCACGGGCTGCTGTCTTCTTATCA
CTGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGAAGTCACTGAGCCTCAATCAAGC
TCTTATCCACAATAACACAGGGAAGGTGATCAGGGAAGGGTGACATCAGGAGTCAAGGCA
TGGACTGTGAAGATGAATCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAAGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACTCAGAAAGGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAATAAGGATTTGAGTTAATTAGCACATGTGAGGG
TTAGACAGATAGGTGAATGCAAGCTCAAGGTTGGAAAAATGACTTTTCAGTTATGCTCTTTG
GTATCAGACATAGCAAGGCTCTCTTGTAGTTCGTGTTAATGTAACTTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

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FIGURE 64

MWLPLVLLAVLLAVLLCKVYLGFLSGSSPNPFSEDEVKRPPAPLVTDEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTATVQSVLLDSAGKACGVSVKKGHELVNIYCPVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYDMDQAMERYVSMPEEAAEH
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTTLTSDES VKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYE EPPKKVRKPALTAIEGTAHG
EPCHFPPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEK WGCETEEEEAAKRRQMQEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSY ALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGG NLIAHMLVLSRL



FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTCTCTGAGCCTTGCTTCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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[illegible]

MT P S P L L L L L L P P L L L G A F P A A A A R G P P K M A D K V V P R Q V A R L G R T V R L Q C P V E G D P P L T M
W T K D G R T I H S G W S R F R V L P Q G L K V K Q V E R E D A G V Y V C K A T N G F G S L S V N Y T L V L D D I S P G K
E S L G P D S S S G Q E D P A S Q Q W A R P R F T Q P S K M R R R V I A R P V G S S V R L K C V A S G H P R P D I T W M K
D D Q A L T R P E A A E P R K K W T L S L K N L R P E D S G K Y T C R V S N R A G A I N A T Y K V D V I Q R T R S K P V L
T G T H P V N T T V D F G G T T S F Q C K V R S D V K P V I Q W L K R V E Y G A E G R H N S T I D V G G Q K F V V L P T G D
V W S R P D G S Y L N K L L I T R A R Q D D A G M Y I C L G A N T M G Y S F R S A F L T V L P D K P P G P P V A S S S A
T S L P W P V V I G I P A G A V F I L G T L L L W L C Q A Q K K P C T P A P A P L P G H R P P G T A R D R S G D K D L F S
L A A L S A G P G V G L C E E H G S P A A P Q H L L G P G P V A G P K L Y P K L Y T D I H T H T H S H T S H V E G K V
H O H I H Y Q C

FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAATCTCCAGGGGACCGCATTCAGAGTCT
 AGTGCCTCTGTGAAGACCCACCATCTACCTCTTGCCACGTTCCACCGGGCTTGGGGGAAAATGTTGGGGACCA
 AGGCTCGGGTGTCTCTCTTCTGGTCTGGAAGTCAACATCTGTGTTGGGAGACACAGATGCTACCCAGTCA
 GTAAGAAGAGTTCAGGCTGTGGGAAGAAGACCCAGCATCTTTTGCCAAAGCTTGCCGACACCTTGAGAGGCTCTGG
 TGAGTGGACAACTATGGTCAACATCTCACTACCCAGCGGGGAAGGGCGATGAGAGCGGTGGAACGCTATCCCT
 TCTACTATGGGACCTGTATCTGCCGCTCCCTGCGCTAGAGACTCGACACACTGACTGGACACTCTGCGGCTG
 AGCATGCGTAGTGTGCTATGGTACTGCCCTGAGGGTCTTGTGGTCTCAACAGGGAGACGGCGCTGGCCA
 GAACTGCTCTAAATTACACCGTACGCTTCTCTGCCCCACAGGATCCCTGCCGCCAGACAGAGCGCATCTGGGA
 GCCCATGGTCTCCCTGGAGCAAGTGTCTAGCTGCTCTGTGTGACAGTGGGTGCGGCTCCAGACTCCGACACCGATTTGCT
 TTGGCAGAGATGGTGTCTGCTGTGCACTGAGGCCAGCGAAGGGTCAAGCTGATGCGGCAGAGCTGTACAGC
 CTGTGACCTGACCTTGCCCAATGGGCGAGGTGATCTGACTGTGATGTGATCTGCTGACCTCTTGACCAAGACCGCGAAG
 ATGGGCTGTCTCCCTCTCCGAGAGTGGCCACGCTCGAGGGTGTCTATCTGACTCTCTGACCTCTTGACCAAGACCGCGAAG
 CTGCTCAOCCAGACAGACAGTATGGAGATTCCGAATCCCTGGCTTTGGCCGTGATGCCAAAGACATCTCGAA
 GATCACAAAGGTCAAGTTTGCCTCCATTTGACTCAACAATGCCCAAGCATAGCTGGAAGCAGCCACCATCAAGG
 CAGAGTTTGTGAGGGCAGAGATCCATACATGGTGATGAACCTGAGACAAAAGACGAGAGCTGGGCGAGAGC
 GTGTCTCTGTGCTTGAAGGCCACAGGGAAGCCAGGGCCAGACAGATTTTGGTATCATATGACATATGCTGT
 GGAATCTGCTCTCTACAGCCTAGAGGACAGAGCTGTGTGCTGAGGAACATCGACAGCACCGCTGAGGAGTACT
 TTTGCAAGGCGTGTCTGTGGGCTGTGAAGCTCTGAGGCTGCTGACAGCTGATGTCACAGCATCTGATGAG
 ACTCTTGTCAACCCAGTCTCTGAGAGCTATCTTATCCGGCTGCCCATGATGCTTTGAGAATGCCCAACATCT
 CTCTACTATCAAGTGGGACGCTGCCCTGTTAAGACTTTGCAAGGCGAGAGGATAATGGGATGAGGCGCTGT
 ATGCTGTGCAAGACTGCTGTGGCATCTCCAAGACAGAGGAAGGAGATCCAGTGTGCTTGGCTACAGCTACCCC
 ACCAAGGTGGCCCAAGGAGTGCAGCTGCGGCGGGTGTACGGAACCTCGGAGCATCTGCGCGGGCGTGTGAGTGC
 TGCTGACATGGGAGCCCATGCGCTTTGGCCATGTATCATGGGAACAGCGCTGTARAGCATGATGCTGCTAC
 AGGCACTTAACTCTCACTCTATCTCCCAAGACACTGAGAGGCTGGTGTCACTTTGTGGACAGGCTGCGAAG
 TTTGTCAACACCCAAAGTGTCACTTTCAACAGAAGGGGAGTGGCGTGTTCATGAATCAAGATGCTCTG
 TCGGAAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAATGTTGTTGGTGAAGACC
 CCTAGGCTGAACTGGAGATTCCATCCAGGAGTTTCTACAGGCGAGAATGGGAGCCCTACATAGGAAGAAGTGAAG
 GCGAGTGTGACCTTCTGGATCCCCGGAATATTTCCAGCCACAGCTGCCAGACTGACCTGACATGATCAATCA
 TGACGAGGAGGACACTTTCCCTCTCGAGCTATGCGATTTCTGTGAGACTTCAGAGATGAGTCACTTCAAG
 AGCACTTAATGCTGCGAATGAGTGAAGTCCACCTTGACTCGACCCAGGTCAAGATGCGAGAGCATCTCCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGTGATTTCAAATTTGAAATCAAAG
 GAGGAACAAAAGAGACAGCAACTCTCTGTTGGGCAACTCGAGATTCTGAGAGAGAGGCTCTTTAACTTGG
 ATGTTCTGTAAGACAGGGCGGTGCTTTGTATGGTGAAGGCTTACCGGAGTGAGAGGTTCTTGCTAGTGAGCAG
 ATCCAGGGGGTGTGATCTCCGTGATTAACCTGAGGCTAGCACTGGCTTCTGTCCAACTTACGGCTGTGGG
 CTCTTTGAGATCTATCAAGAGGCCCAAGGGCCCTGTGCTCTGTGATGACCATGCTGATGACCAAGTCCCTGTATG
 CCTATCTGCTTATGCTCTTGGCAAGCCCTGGCTGGGAGGAATCGAAGCAGTGAGGTCTTCTCTAAATTTCAAC
 CCAAAATGCAATTTGGCGTCCCTCAGGCCCTATCTCAACAAGCTCAACTACCGTCGAGAGGCCATGAGATCCAG
 GGTTAAGAAACAGCTTCCAGATATAGCATGGCCAAAGCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCGCA
 TCTATGCTTTGAGAACTCCGGGCATGTGAAGAGGCACCCAGTGCAGCCCACTTCCGGTCTTACAGATT
 GAGGGGGATTCATATGATCAACACACTCTCTCTCAAGACAGCACTGATGATGAGCTGGAGTCAAGTATCT
 GGCATGCTGGCCAAAGCCGATGGAATTGAGGCGCTGCTATATCAAGGTGAAGATTGTGGGGCCATGGGAATGAT
 ATGTGCGATCCCGCAACTGGGGGCATCTACGCGGACAGCTGATGGAATCCAGATGTGAGG
 AGCATCTGGGACAGGAGACAGCCCAATGTCTCAGCTGCTCTGTGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCGAGACGCTGTGGACCGCACCTGGTGAAGGCTCATCCCCAGGGCAGCTGCGTGGGCGAGTGTGAACCCCA
 TGCTGATGAGTACTGTTCAACCACTTGCCACTTGCAGTCAACACAGCACAGCTGATGATGACAGCTGTGSCA
 CCTTGGACATCGGACACTTATGATATGTCATCTGACCTCACTCAACAGGAGCCCTCGACGCGCAAGGAGAT
 CGCGCTCGGCGGGTCTTTGATGGCACATCCGATGGCTCTCTCAGAATCATGAAGAGCAATGGGAGTAGGCC
 TCACCTTCACTGTGTAGAGAGGCAAGTAGGCGCGAGGTGCTTCCAGTACTCTCAAAGACCCCCAGCCAG
 TCCCCGTCTGCGAGCATCTCTCAAGGAAGATGCCCTCGAGGAGGCAGCAGGAGGAGCGAGGGTGGCCACGG
 CGAGGTGGAGTGGTGGCTCTCTGAGATTCTCTAGAGTTGCTCAACAGCCCTGATCACTCAAGTTTGTGG
 ACTTCACTCTCTGCGCTCATTTTCTATGTGACAGCCATGTGAGCTGTATGACAGAACTGCTGACTGATAT
 TTAGACATCTGCTGCTGATGATGCTGTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT
 TTGSCAGCTGGCCCCCAATGGACAAATAAGGCCCTTTGTGAAACTGTTCTTGAATGAACACAGAAATTT
 GGGCACTGGTAAACTCTGACGTTCTCACTGTACTTCAATTAAGCCATTAAAGAAATATCTCTCTTCTT
 TTGTCATGCTTTTGCCCACTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATATAAGCATAT
 TTTCTGGGCTTGTGTCACAGGACATAGGCAGGCTTGTATCATCTATCATATAAATGGGTGGTGAATAAG
 AATAAAGACCAATCTTTGATGTGAAGTGAATATATTTCTTTGCTAAATTTGGAATCTGAACTCTGAT
 ACTTCAAGTTTAGCTATTAATATAGGTGATCATAGTTCCCTTACCAAGTCTGGAAAGAGACTCTCGGTG
 ATCCAAATTTACACAGGTTGCTAACTGATTTGTACATTTCTCTTGCATTCGTTTGTCTGTCTGATAGAAAC
 CCGAGTGTAGCCAGGGCAGATGTCAATAAATGCATCTCTGATTTTGGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTFAGSTGQVVHGSREGFWCLNREQ
 RPPGQNCSNYTVRFLCPPGSLRRDTERIWSPPSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDSDGRFRIPGLCPDGKSIILKITVKVFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPESYLIRLPHDCFQONATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPTITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPNISTATAAQTDLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNIAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAFAQISMAKPRPNSAEESSNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDINTVFPN
 EDDPMSWTEGYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLVKVIPPQGSRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACAAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTGGTTTGGGATCTGCTTGGAGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAGAATTTAGAGATGATTGTCAAGATCCCTGCGATTATG
 CCCTTTGGSTAGCGGTGTCCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGACATTATGATTGTGTAAGACT
 CAGATTTACACCGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAAACTCGATCTCTCGGATATTACCTTGGAGACCTCTCGAGACCTCTGAGACCTGCTGTGCAATGGGCAT
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACCCCCCTGAGCTGATGTTGATT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCTCTCCAGGTTAACT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAAACAAAGAACTCAGAGATTTCTTT
 ACAGTCAACAGACTGAGGATAAGGCTGTTAAGACCGACGCTGGGGGAAATTTGTAGATGAGTACACTTGGC
 ACGCTACTTTTACGGATCTCAGACATAAAGTGCAGGAAGTGCAAGTGTAACTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAATTGACATGCGAATGTGAGCACAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTTACAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGACTGCAAACTCCTGTATCCC
 CAGTATTTCCAGTATTGTCAGAAATGTCTGCGACAACGAGCTCCTGCACTGCCAAGCGAGGAGCTGCCACA
 ACAAGCTGCGCTGCTGTGCCCCGCCATACACGGGCATCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCAGCGCTGTGCTGCTGACCACTGCT
 GGGACCCGCCAGCCCCCTGGTGTCTAGGTGTCACTCCAGCCACACCGGACGGGCTGTGCCCTGGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACTAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACTCCGAGTCAAGACTGTTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAACTCAACCGACCTAAAAACATTTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGTGTCAG
 GTGCATTGTGGGCATAAGGAAATCTGTTACAAGTGCATATTGGCTGCTTCCGTCCTGAATCCCTTCCAAC
 CTGCTCTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTCTTTGTGCTGATGTTAGTGATGCA
 TGTGTAACAGCCCCCTCAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCATGAGTCCAGTGGCA
 GCACACACCCATATACAGAGTGGCTATAGGAAAAAGAAAGTGATATCTCTTTGTATTCAAATGAAGTT
 ATTTTCTTCTGAACACTGTAATATGTAGATTTTGTATTATTGCCAATTTGTGTTACAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAGAGCTGACATTTTATTGTCCTCTTCGTTCTGTTTGTCTACTGTGCA
 GATTCTCTGTGAAGGCAACGACGCTGCTGGCATCAAAGAATATCAGTTTACATATACAAAGTGTAAATA
 TTCCACCAAGGACCTCTAAATGTTTCTTGTGCTTTTAACTGGAAGATTAAAGAAATAAAACCTCTGCA
 TAAACGATTTCAGGAATTTGATATGCAATTTCTTAAGTGAAGGAACGCCACCAAGCAGTTTTCACACTCT
 TTAATGATTTCTGTGGACTGAGTACATTACGTGACGAATTAAGTCCCGAGGAGTGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACACAGCAAAAAAAAAAAAAA
 AAAAAA

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGCTCCGGGCGAGGTGTCTCATGACTT
 CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTGTCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGAGACCCCTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTCACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTC**G**TGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTATATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTATGTATACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAACTCAGTAGTACAACC
 TAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTATATCCTATGTATAAATAAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTATTAACAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 77

TGCTTCCTGGAGACCCGTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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FIGURE 78

CTCAGCGGCGCTTCTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAGGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGTAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCGCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCTTTGCATATTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCACTCATGCATCTCCTTCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTAGACATGGAGCTG
 CTACACAGACAGTCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCCGAAGGC
 TTAGCCTGGCAACGGAACTGGGCTACCCCTGGCTATGCTGTGCTTGGTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGTGTCTCATCGATGAGGCTGCCATG
 CCCCAGGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCACTCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCTGCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGACAGCCTTTGACGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCCGCTGCCGT
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCACT**AGTGA**CTCCAGCTGGGGGTGGGA
 AGGAAAAAAGCTGGACACTGCCATCTGCTGCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAACTCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATT
 GCATAATCTGAGCCAGAGTTTGGGACAGGACCTCCTGCTTTTCCATACTTTAACTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCAAATCTGTTTACATCA
 ATCTGCCCTCACTGCTGTTCTGGGGCATCCCCATAGCCATGTTTACATGATTGTATGTGCAAT
 AGGGTGGGTAGGGGACAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 TTTGCTCTGCGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCFTTLAIALGAVLLLPPFSIISNEVLLSLPRNYIYQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGIFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDGFRFNWLGIFY
IVFLYNAAFAGLTTLCVLKFTTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

[illegible][illegible]

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTG
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCAGACTGCCCCGAGTTT
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

Parameter	Estimate	Standard Error	z-Statistic	p-Value
Intercept	1.0000	0.0000	1.0000	0.0000
Age	0.0000	0.0000	0.0000	0.0000
Gender	0.0000	0.0000	0.0000	0.0000
Marital Status	0.0000	0.0000	0.0000	0.0000
Education	0.0000	0.0000	0.0000	0.0000
Income	0.0000	0.0000	0.0000	0.0000
Health	0.0000	0.0000	0.0000	0.0000
Religion	0.0000	0.0000	0.0000	0.0000
Occupation	0.0000	0.0000	0.0000	0.0000
Residence	0.0000	0.0000	0.0000	0.0000
Time	0.0000	0.0000	0.0000	0.0000
Constant	0.0000	0.0000	0.0000	0.0000

[illegible]

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCTTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGCGGAGGAGGTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGACGAGATTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCTCTATAAAGGATATTAAAAAGGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCAGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCAACCCAGCTGGGCGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTTGAGAGTG
 AATAAAATTTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTCATTTCGGAAGAAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGCTCTGGTCTGCCGCTGAGT
 TTCAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTG
 TTATTTTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQ
DRNI PRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKNCRQEMRTTQLGPGRFQ
MTQEVVDCPCPNVKLVNEERTLEVEIEPGVRDGM EYFFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHK VHSRDKITRPGAKLWKKGEGLPNFD
NNNIKGS LIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGCCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATTAAGATTTTGGGGTGCCNTGAAGTGCCNTNTATAAAGGATATTA AAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCCGAACCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTNTTTTGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGGGGGCGAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAAGTGTGCTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGCCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGGTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTCTGCAGGAGCAGTCTGCAATT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTCTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACGTGGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGAGCTGTGAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAAGAGGAGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAT
 ACAAAGTTGATGATTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACCTAGGTG
 GATAGTAAATTTATACTTATGTTCCCTCAAAAAAAAAAAAAA

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTTCCGTTCCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTGTTCAG
GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAATTTGAAGACTCATTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAAGGCTATTTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCGTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCACATGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTNGNCNAGGGCC

FIGURE 90

MISLTDQTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGACAGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCTTCTGAGTCTTGGATCTTTCTTCCCTTCTGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
 TGAAGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCCTCAGGGCTAATC
 ATCAACACCATTAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCAGGAATGCACCATCTTCACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTGGCCACCAGTTTGACGACCTCCGGGACTACCCGAGAAGTATTTTTTCTCT
 GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
 TAATGAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCGA
 GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCTTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCTGACG
 CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGACAAGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAGGTGCTTTAGGTGAGATGACTAAATTATGCCTC
 CAAGAAAAAAATTAAGAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGCGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTTGGGGAA
 GTAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTCATTGATCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCCGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAAACAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAACACGAGAAATTGAGAAAAGGAGAGGAGCAGATTCAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCAAATTCGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACACACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTAAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAAGTAAACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTCACCTTTCCTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCCTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAAATCTCCTTAAAG
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATTTTTTTTTTTTTTTTTTTTTT

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSPLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDDVNDLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

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FIGURE 96

GGCAGCGCCGCGCGCGGAGGGCAGAGTCAAGCCGAGCCGAGTCCAGCCGAGCAGCGGACGAGCGGACGAGCGAGGGCAGC
 CCAAGCAGCGCGCAGCGAAACGCCCGCGCGCCACACCCCTCTGCGGTCGCCGCGGCGCCTGCCACCCCTTCCTC
 CCTTCCCCGGCTCCCCGCTCGCCCGCCAGTCAGCTTGCCGGGTCGCTGCCGCCGGAACCCCGAGGTCAACCA
 GCCCGGCGCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTCTCCCTCGCCCGGCGCCTGGCACC
 GGGGACCGTTGCTTGAGCGCAGGCCACGCTACTTTTCGCCCGCGCTCCTCCGCTGCTCGCTCTTCCAC
 CAACTCCAACCTCCTCTCCTCCAGCTCCTCTGCTAGTCCCGGACTCCGCGAGCCCTCGGCCGCTGCGGTAG
 CGCGCTTCCGCTCCCGTCCCAAGGTGGGAACCGTCCGCCCGCGCGCACCTAGCGCAGCGTTGCGCTTGGC
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAATTGCTCGG
 AAGTGGCAGCTCTTACGTGTCCAAGGCTTCAACAAGAACGATGCCCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAGATAAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTCAGGTTACAAGAAGTTTG
 ATGAATCTTCAAGAATACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTGTAGAGTTGAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT
 CGCAATTTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGCTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCAAGCCCTCCCGCTGGACGAAT
 TCTCGTTCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACACAGC
 AGCTGGCACTAGTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCT
 CCCTTCGCGCAACGTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTTCAGTGACAGGAAATGGATAGCCCAACAGGGCAACCAACCAGAGGTCCA
 GGTTGACACCGCAACACGACATACTGATCCTCGTCAAAATCATGGCTCTTCAGTGATGACCAAGATGA
 AGAATGCATACAAATGGGACGACGTGGACTTCTTTGATATCAGTGATGAAGTGTGGAAGGAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCATGA
 GAAAGCCGACAGTGCTGGTCCGTCCTGGGGCACAGGCCATACCTCCTCACTGCTCTGCTATCTGTTCTCTGG
 TTATGCAGAGAGTGGAGATAAATTCACAACTTCAGAAAAAGTCTTCAACAAAAGTTAAAAGGCACCAAGT
 ATCACTTTTACCATCTAGTGACTTTCCTTTTAAATGAATGACACAAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAAGTCTGACTTGTGTTTCTCATTCAGTTTGGGAGGAAAAGGACGCTGCATCTGAGTTGGT
 TCTCTGCTCCCCCAAAACCATGTAAACGTTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTGTGCAATTTGTA
 TTATACACTATATTATTTGTTGTATCTTTTTCATTCAGTTTGGTGTGGGTTTCTTTCACACTGTGATCT
 CGCTTGTCTTACAAAGCAACAGGGTCCCTTCTTGGCAGCTAACATGTAGTATTTCTGAAATATTAATA
 GCTGTACAGAAGCAGGTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGCPPKPLPAGRISRSISESAFSARFRPHHPPEE
RPTTAAGTSLDRLVTDVKEKCLKQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTTTGTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTATTAACTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
 AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
 GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
 AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
 GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
 TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
 CTGACTGCATTTTGGCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
 ATGGAGAGGAAA

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FIGURE 101

MAVLVLRLTVVLGLLVLF~~T~~CYADDKPKDPDDK~~P~~DDSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTGCTTCTTAC
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGCGAGCAAGTTTTCGAGCCCCACCTGGAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCAATCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCTCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAACCTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCGAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTTGTGCA
 AGGTGATATTTCTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAAACGATATTCAACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAAACATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCTCGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGAAAAAGATGTGTGAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGTTACAGA
 TAATTCAAACCTGCTGTTGGTTTTAATTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIGHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDI LALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 106

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGACAGGAACCGGGCGGCAGACAAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCGGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCCCGAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAACGACAGAATATACTAACCAACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACCATGATTTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAATAATGTTATTTCCA
 GACCCAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAAATTTGAACGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCCTCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCAATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTCTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTGGGGAAAGCAAAGTGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTCTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAAA

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCAGTGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGAA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCAACACCCCTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTCGTCTTGATTTTTGTTCTCAGAAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTCTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGAATATAAGCCCT
 TTCGGGCATTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCGTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGAT**TAGAT**ATCCCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTAAAGACCTAATAAACCTATTCTTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWYSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFII FLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATTAATTTGTATGGGATTTGTGATGCAGGAAGCCTAAGGGGAAAAAGAATATTCATTCGT
 TGTGGTGAATAATTTTTGAAAAAAAATTTGCCCTCTTCAAACAAGGGTGTCAATCTGATATT
TATCGAGGACTGTTGTTCTCACATATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGTCTGG
 TGACTGGAGTACATTCAAACAAGAAACGGCAAGAAGATTAAAAGGCCCAAGTTCACTGTG
 CCTCAGATCAACTCGCATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGCCCAAAATACCATGTTTATGGCACTGAGGTATGCATCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGAGGGGAAAAATCTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAGGGAGTTATTCCAACGGTGTCCCAATCGTT
 ATCCCTACCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA
 CCTACCCTCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 TGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCCAAGGCCATCCCTCTTG
 CTGCTTCTACCACAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCAAAACAGGCCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTGAGCCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTGTGCTTTTTAATGTATGGGAGCACCAGCATTTGGCAAAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTTGGCCCTGCCGGTCCAC
 TGATGGGTGTGTTCCAGATGTGAGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCGGGCCATCTCCTTTGTGACCAGAAGTCTTTTCCAAAGCCCAATGGAACAGAAAGCG
 GGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCCAAGGCAAAAGTGGAGGAGGCT
 TCAAGACTTCCGAGAGAGATCAGGAATCAACATTTTCTTCATCACCATTGAAGTGTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAGGCCGTGTGCAGAACAAAGC
 GCTTCTACTCGCTCCAGTGCAGAGCTGGTTTGGCCTCCCAAGACCTGTCAGCCTCTGGTG
 AAGCGGGTGTGCGACACTGACCGCCTGGCTGCGAGCAAGACCTGCTTGAACCTCGGCTGACAT
 TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGACGGGCAACTTCCGCACCGTCTCTCCAGT
 TTGTGACCAACCTCAACAAAGATTTGAGATTTCCGACACGGACACGGCCTATCGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCCACGACACGGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGATCACCTATGCGATAGGCGTTGCCTGGGCTGCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCGCCAGAGACCACTCCTTCTTTTGGACGAGTTTGACAACCTCATGATCATGTG
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTCAAG
 CAGGCAGAGCACCAGCAAGTGCTGCTTTACTAAGTACGCTGTTGGACACCCCAACCGCTTAA
 TGGGGCAGCGACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTTGTATTAT
 TTCTTTGGCATATGCTTTTTTATATTCCAAACTTGAGTTTACAAGATGATCACAAACGT
 ATGAGATTGAGCCAAAGGCTACATCATGTTGAGGGTGCTGGAGATTTTACATTTGACAATT
 GTTTTTCAAAATAAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTGTGTTATTCTGATTGAAGCTCTGTAACCCCTCAGCAAGTTTCAATTTT
 GTGATGACAAATGTAGGAATGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAA
 AA
 AA

00989731.112011

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTVGHSNKETAKKIKRPFKFTVPQINCVDKAGKIIDPEFIVKC
 PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
 SLPRWRESFIVLESKPCKGVITYPSALTYSSSKSPAAQAGETTKAYQRFPPIPGTTAQPVTLMQ
 LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQ
 RQDPSGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
 IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKLTHTNSRDLKTAIEKITQRGGLSNV
 GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
 NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
 GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDSTDTRIGAVQYTYEQRLFQFDKYSSKPDIL
 LNAIKRVGYWGGTSTGAAINFALQLEFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
 VITYAIGVAWAAQEELEVIATHPARDHSEFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAACAACTT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTC
 TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCCGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGAGGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCTCACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTAC
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATA**TAA**CACTGGATAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHAGAPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSLEAYWPGQLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTACAAATGTTTCTAGAAGAAATCTGGACAAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGGCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTGTCGCACTGTTGCTGTGGAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGGTGG
 TGGTCTCCAGACACCTTGAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCAGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCAT**TAG**GTTTGCAGAAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGTGCTGAGCAACC
 CTGGGAAAGTGACTTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTCTTCTGGAGAGCAGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTCCAGATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAATGGGATGTGCATGAACCGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCACTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHPPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREP GAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFM LILV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGTCCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNCGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGTGGCGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTGAGTGGAGGAGGTGAGCCCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATAACACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAATAGGAACCTCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAACAAAAATGTGTGGCAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAAATAGGAGGCATTCAATGAACATTTTTTGCAATATAAACCAAAAAATAACTTGTATCAAT
AAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAAATACCTCAGCATATAAAATAAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGCGCCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGTTCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTAGGTTGACCTTTGCCAACTCAAGGAGGAGGTTGGACAA
 AGCTGCTTCTGGCTCTCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGTCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAAGCTATGGAAGTGGAGTATGTCTCAAGAAGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCACTACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCTCTGCTGCCATG
 ACCCATCAACATCCAGTTTCACTCGGGGACAAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGGCAG
 GCACAATGATGTCTGATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATTGGC
 AAGAAGGCATCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCAGAT
 GTTCTGGACATTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCTTGTGGTGGCTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTGTCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACTCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCCTGCATTGCGCTGAAGGACGGGGAGGAGACACGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTGTGCACAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATCAAACCTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCCAGTTT
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATCAAGAGCTCCTGGATGGGTG
 CGGGAAGTCGCTGGGCACAAGGTGCCAAAGGCAGGCAGCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCGCCCTGTCTGCTCTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQP GALKSQRLPDLTTVISVDAPLPGTLLLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSVPVTFHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKINTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCKIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCAGTGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCAGTTATGACATCTCGACCATGTGTGGAGGTGTATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATGAAGGACCTGGTGGT
TGCTTATGAACCACAGAGAACAGTCCCCTGACATTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGATGTGCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGG
 GTGGACGCTGCAACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTTCGGGACTCCCGGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTGCGAGGGGTCCCGCTGTAACT
 CTGACCTCCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTACGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCGTGCGTGTGGTGTCTACTGT**G**
AGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTGGGAAATAAAATACGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTGGAGACAGCTCCTGTATCCTTCTCATCTTGTCTC
 TCCGCTTGCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCFDGNVTLTAANVT
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKMPAPT SQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL



CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGACGCTGTCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCTTTTCATTATGATTACCAGACCTTGAGGATTGGGGACTGGTGTT
CGCTGTGGTCTCTTCTCGTTGGGATCCTCCTTATCTTAAGTCGACAGGTGCAAGTGCAGT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCACAGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAATGTCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCCTTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCTGCAGCCTGCGGTCTT
GCCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCTTTGTGGCTACTTGTGTGTGGATGGTATTGTGTTTGTAGTGAACCTGGGACTGCGTT
CCCAGGCAGGGGCTGAGCCATGGCCATGACCTCCCTGCCCGTGGCCCTCCATCAC
CTTCTGCTCTTAGGAGCTGCTTGTGCCCGAGCAGCCCTCCCTGATTTAGGGATGC
TAGGGTAAGAGCAGGGCAGTGGTCTTCAGTCGCTTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTGCATCATTTCTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTATCCC
ACCTGATCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTGAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCACG
AGGAGTCCCCTATCTGCCCCGCCCTTTCACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCTTGGGAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCTGGTGGTCAG
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
GTTGAAGGTCATAACGAGAGTGGGACTCAACCCAGATCCCGCCCCCTGCTGCTCTGTGTT
CCCGCGGAACAACCAACCGTGCCTGTGACCAATTGCTGTCTCTGATATCGTATCGTATCTAT
CCTCAACAACAACAGAAAAAAGGAATAAAATATCCTTTGTTTCTT

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTQVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTTCATCCAAA

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPKLGKGLRSATPDAQ

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FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTATATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCTTCTGCAGCTTCATTGATTTTGTATATC
TTCATATTAATTGTAACGATTAATAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

100
90
80
70
60
50
40
30
20
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100

FIGURE 132

GGGGAATCTGCACTAGGCTCTGCCGCGCATGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGCGGCCAGAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAATTAACAGGCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGCTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTCTGTCTCGGAAAAACCCAAAACCTTGTGTATGCAGAATACACCAAAAAC
 CAGGCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCAATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAATGAACTATAGTAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGTGTCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCACCTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC
 ACAGCTGTGCTCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAACCATAAAGCTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLPSAQGRQKESGSKWKVFDIQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPVVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSY
NVTRRKG YDQIIPKMLKTEL

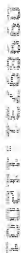


FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**CCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACAGCTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAGAAAACCTCCACCTGCTCTCTCGGCCCGAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCTCCCACCTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGTGTCCCTCCA
 GGCCCCAACCTTGCTCTACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CTGCTCTCCCGAGGAAGATGCTCTGCAGGAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRF TSLRPLLGGIPESGGPDARQGWL AALQDRSILAP
LAWDLGLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLHRHPVCVELLTVLWVPTLGTDRLLLAFLTLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCTCGCTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTACACACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGCTCTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCTGTGCTGTCACTCTGAGTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAACTGCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGCTCTTGGTGGGGATATGAGGTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
 ATTCAGGTGGGTAAGTGAATTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATCTGCAGTGGGTTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCCAAGGATCTATGAAATGATGGGTACAGTAAACCCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTGAATTTATTAAGTGAACATTCATATTCAGAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTATTAAGCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGAAA
 GTGTTAAATAAAGTAGGTACTGTGAAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATGGAGGTTTTTGTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCACTCTGTAGACTAGAATTTCTTAAAGGG
 GTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTATTG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATCTTTACATGCAACATTTTCCAGTTACTTAACGTATCAGTTATTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGTCATTATTGCATATCAGTAATCTCTTGGACATTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
 FHFTLREHSNCSSHQNPFLVILVTSHPSDVKAQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
 EDKMLALSLEDEHLLYGDII RQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
 TGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPFYCSGLGYIMSRD
 LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNHIHPEDTNLFFLYRIHL DVCQLRRVIAAHG
 FSSKEIITFWQVMLRNTTCHY

$\begin{bmatrix} a \\ b \end{bmatrix}$
 $\begin{bmatrix} c \\ d \end{bmatrix}$
 $\begin{bmatrix} e \\ f \end{bmatrix}$
 $\begin{bmatrix} g \\ h \end{bmatrix}$
 $\begin{bmatrix} i \\ j \end{bmatrix}$
 $\begin{bmatrix} k \\ l \end{bmatrix}$
 $\begin{bmatrix} m \\ n \end{bmatrix}$
 $\begin{bmatrix} o \\ p \end{bmatrix}$
 $\begin{bmatrix} q \\ r \end{bmatrix}$
 $\begin{bmatrix} s \\ t \end{bmatrix}$
 $\begin{bmatrix} u \\ v \end{bmatrix}$
 $\begin{bmatrix} w \\ x \end{bmatrix}$
 $\begin{bmatrix} y \\ z \end{bmatrix}$
 $\begin{bmatrix} a \\ b \end{bmatrix}$

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNDNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAAATTTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTAC**ATGA**AATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTCCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGCGGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCCTCA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATGCGAGACACTGTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTTACAAGGAAATAAAATACAAAT
 CTGTTTTTTCTAAAAAAGG

MNDSLRTNVFVRFPQETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRVKQALQEAQLKAKGLNPDGTPALSTLGGFSPASKPSPPREVKAEK
SPISINVKTVKKEPEDRQQAASKSPVNGVRKDSKRSRNSRASASRSRSTRSRSHSTPRRHH
NKRSRSGTYSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSNRHHGHRKKRSRBSQ
SSRSRSDAAKKHRHREGHHRDRRERSRSFERSHKSHHGGSGRSGHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTACAGAAATATAT
TANCTTTTATAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAATNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAAGCAAAGGGATT
GAATCCGGATGGAACCTCCAGCCCTTTCAACCTGGGTGGATTTTCTCC

FIGURE 143

GGACAGAGGCTCGTGCCAAGCTTGGACAGAGGTGCACCGCTTCTCGCACGCGTCA**ATGGC**
 GGTCCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCTCATGCACAGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTGTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCTCACCTTTGCTTCTCTCTGCTGCTGGCCATGCTGGTGAAGTGGTGGC
 GGAGGAGACCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCCTGCGGTGGC
 CCAGACCCACCGGAGCAGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCAAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTCACGGGAC
 TTCTGTCACACAGCCGCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA
 CTCTGGGCGCCTCTGGTGTGCTGGTGTGCTGCTGCGCTGCGCGGTGACCCGGCCCC
 ACCTGCAGGCCCTACCTGTGCCGTGCCCAAGGCCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
 GGCTCCT**TAG**TGCTGCTGACAGCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GGCGTTCCCTTACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTF AFLFLLLAMLVQV
VREETLELGLEPLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVVRVYCYVT
VVS LQYLTP LILT LNCT LLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA GS



FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
 CGCTCTCTTCTGGTCTTGGCTTGGCTCAGTCTCTGCTAACTACATGACAATGTGGGCAACTGCACTTCTCTG
 TATTGAGAATCTCTAAAGGTGCTCCCACTACGGCTGACCAAGATAGGAAGAGGCGCTCAAGAATGGCTG
 TCCAGACGGCTGTGGAGCCTCACGCCACGGCTCCCTCCCAAGAGTTTCTGCAGCTGCCACCATCTCTTTAA
 TGACAGACGAGCCTGGCCTAGACAAACCTGGCTACGTGTCTTCGGCAGAGGACGGCGACGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAATAAATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACGAGG
 GCAGGGAAAATTTGAAAAACCACTGCCCTGAAAGTCTTTCCAAGGTTGTACCACCTGATTCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCCAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTAGCTGTGCGTCTCCTGGCG
 CAGCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGCAGCAGGAACAAATGGACAGGCCCC
 GGATGCCTACAGACCCCGAGATGACAGCTTTCTGTTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAATCGTGGCGCAAGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TGCGGCTCATCTGATTACAGGCCAGTGAAGACGTGTTCACTCGTGTCCCGCCAGGTTCCGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGACCAACT
 CCCAAGCCCTCCATCTACAACTACTTGTGATGAGAAGGTGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGGAGCATCACATAGAGAATGGGATTTGCTATCTATGTCATCAGTGTGTAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCAACTGACA
 GAGGTGAGCGGAGTGAGGCAGTGGCATTTATGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGATGATGAGCCCAGGAAGATGCAGCAGCCAGCAGCCCTGGACTCCAACCAACACATGGCCCCACCCA
 GTGACTGGTCCCATCTGGGTCATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGAGGAGGTTATGAAGAATACAAATGGAAACAAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACAGCATACATGATGGAAGAATTAGATGTGGTGATATCTCTTGT
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTCTTGGCCTGGCACTTTTTTATGAAGATCAATGATGGGTGAGAGGAAAACAGAAAAA
 TCAAAATAGGCTAAGAGTTGAACACTATATTTATCTGTGAGTTTATTTAAAGAAAAGAAATACATTGT
 AAAAATGTCAGGAAAGATGATCATCTATGAAAGCCAGTTACACCTCAGAAAAATGATTCCAAAAAATTA
 AAATCTAGTTTTTTTTCAAGTGGAGGATTTCTCATCTACTACAACATTGTTTATATTTTTTCTATTCAAT
 AAAAGCCTAAAACAACTAAATGATGATTTGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGCTCGCAAGGTACATTATGGCCATTTTAAATTACAGCTAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTGCTTTCTATCAACAAGAAATAATTTTTTCAGAGTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPVESAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAFEVFFRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHLIQASERRVHLVVSQRVQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFIFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCAGGCAAATG**GTG**GCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTT**TAGG**ATGATTAGCCCTCTTGTTTTATCTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCCTTCCCAATGCCCACTAATTTTGAGATT
AGTCAGAAAAATATAAATGCTGTATTTATA

FIGURE 150

GGCACGAGCCAGGAAGTCTGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGAAGTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCGG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCAGAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
 GGGTTTCAGGATAGGGAATGGGGAGGTGAGAGGACGCAAGCAGCAGCCATG**TAGA**AATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAAA

Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* on the substrate. The concentration of the spores was 10⁴ spores/g (a), 10⁵ spores/g (b), 10⁶ spores/g (c), 10⁷ spores/g (d), 10⁸ spores/g (e), 10⁹ spores/g (f), 10¹⁰ spores/g (g), 10¹¹ spores/g (h), 10¹² spores/g (i), 10¹³ spores/g (j), 10¹⁴ spores/g (k), 10¹⁵ spores/g (l), 10¹⁶ spores/g (m), 10¹⁷ spores/g (n), 10¹⁸ spores/g (o), 10¹⁹ spores/g (p), 10²⁰ spores/g (q), 10²¹ spores/g (r), 10²² spores/g (s), 10²³ spores/g (t), 10²⁴ spores/g (u), 10²⁵ spores/g (v), 10²⁶ spores/g (w), 10²⁷ spores/g (x), 10²⁸ spores/g (y), 10²⁹ spores/g (z), 10³⁰ spores/g (aa), 10³¹ spores/g (ab), 10³² spores/g (ac), 10³³ spores/g (ad), 10³⁴ spores/g (ae), 10³⁵ spores/g (af), 10³⁶ spores/g (ag), 10³⁷ spores/g (ah), 10³⁸ spores/g (ai), 10³⁹ spores/g (aj), 10⁴⁰ spores/g (ak), 10⁴¹ spores/g (al), 10⁴² spores/g (am), 10⁴³ spores/g (an), 10⁴⁴ spores/g (ao), 10⁴⁵ spores/g (ap), 10⁴⁶ spores/g (aq), 10⁴⁷ spores/g (ar), 10⁴⁸ spores/g (as), 10⁴⁹ spores/g (at), 10⁵⁰ spores/g (au), 10⁵¹ spores/g (av), 10⁵² spores/g (aw), 10⁵³ spores/g (ax), 10⁵⁴ spores/g (ay), 10⁵⁵ spores/g (az), 10⁵⁶ spores/g (ba), 10⁵⁷ spores/g (bb), 10⁵⁸ spores/g (bc), 10⁵⁹ spores/g (bd), 10⁶⁰ spores/g (be), 10⁶¹ spores/g (bf), 10⁶² spores/g (bg), 10⁶³ spores/g (bh), 10⁶⁴ spores/g (bi), 10⁶⁵ spores/g (bj), 10⁶⁶ spores/g (bk), 10⁶⁷ spores/g (bl), 10⁶⁸ spores/g (bm), 10⁶⁹ spores/g (bn), 10⁷⁰ spores/g (bo), 10⁷¹ spores/g (bp), 10⁷² spores/g (bq), 10⁷³ spores/g (br), 10⁷⁴ spores/g (bs), 10⁷⁵ spores/g (bt), 10⁷⁶ spores/g (bu), 10⁷⁷ spores/g (bv), 10⁷⁸ spores/g (bw), 10⁷⁹ spores/g (bx), 10⁸⁰ spores/g (by), 10⁸¹ spores/g (bz), 10⁸² spores/g (ca), 10⁸³ spores/g (cb), 10⁸⁴ spores/g (cc), 10⁸⁵ spores/g (cd), 10⁸⁶ spores/g (ce), 10⁸⁷ spores/g (cf), 10⁸⁸ spores/g (cg), 10⁸⁹ spores/g (ch), 10⁹⁰ spores/g (ci), 10⁹¹ spores/g (cj), 10⁹² spores/g (ck), 10⁹³ spores/g (cl), 10⁹⁴ spores/g (cm), 10⁹⁵ spores/g (cn), 10⁹⁶ spores/g (co), 10⁹⁷ spores/g (cp), 10⁹⁸ spores/g (cq), 10⁹⁹ spores/g (cr), 10¹⁰⁰ spores/g (cs), 10¹⁰¹ spores/g (ct), 10¹⁰² spores/g (cu), 10¹⁰³ spores/g (cv), 10¹⁰⁴ spores/g (cw), 10¹⁰⁵ spores/g (cx), 10¹⁰⁶ spores/g (cy), 10¹⁰⁷ spores/g (cz), 10¹⁰⁸ spores/g (da), 10¹⁰⁹ spores/g (db), 10¹¹⁰ spores/g (dc), 10¹¹¹ spores/g (dd), 10¹¹² spores/g (de), 10¹¹³ spores/g (df), 10¹¹⁴ spores/g (dg), 10¹¹⁵ spores/g (dh), 10¹¹⁶ spores/g (di), 10¹¹⁷ spores/g (dj), 10¹¹⁸ spores/g (dk), 10¹¹⁹ spores/g (dl), 10¹²⁰ spores/g (dm), 10¹²¹ spores/g (dn), 10¹²² spores/g (do), 10¹²³ spores/g (dp), 10¹²⁴ spores/g (dq), 10¹²⁵ spores/g (dr), 10¹²⁶ spores/g (ds), 10¹²⁷ spores/g (dt), 10¹²⁸ spores/g (du), 10¹²⁹ spores/g (dv), 10¹³⁰ spores/g (dw), 10¹³¹ spores/g (dx), 10¹³² spores/g (dy), 10¹³³ spores/g (dz), 10¹³⁴ spores/g (ea), 10¹³⁵ spores/g (eb), 10¹³⁶ spores/g (ec), 10¹³⁷ spores/g (ed), 10¹³⁸ spores/g (ee), 10¹³⁹ spores/g (ef), 10¹⁴⁰ spores/g (eg), 10¹⁴¹ spores/g (eh), 10¹⁴² spores/g (ei), 10¹⁴³ spores/g (ej), 10¹⁴⁴ spores/g (ek), 10¹⁴⁵ spores/g (el), 10¹⁴⁶ spores/g (em), 10¹⁴⁷ spores/g (en), 10¹⁴⁸ spores/g (eo), 10¹⁴⁹ spores/g (ep), 10¹⁵⁰ spores/g (eq), 10¹⁵¹ spores/g (er), 10¹⁵² spores/g (es), 10¹⁵³ spores/g (et), 10¹⁵⁴ spores/g (eu), 10¹⁵⁵ spores/g (ev), 10¹⁵⁶ spores/g (ew), 10¹⁵⁷ spores/g (ex), 10¹⁵⁸ spores/g (ey), 10¹⁵⁹ spores/g (ez), 10¹⁶⁰ spores/g (fa), 10¹⁶¹ spores/g (fb), 10¹⁶² spores/g (fc), 10¹⁶³ spores/g (fd), 10¹⁶⁴ spores/g (fe), 10¹⁶⁵ spores/g (ff), 10¹⁶⁶ spores/g (fg), 10¹⁶⁷ spores/g (fh), 10¹⁶⁸ spores/g (fi), 10¹⁶⁹ spores/g (fj), 10¹⁷⁰ spores/g (fk), 10¹⁷¹ spores/g (fl), 10¹⁷² spores/g (fm), 10¹⁷³ spores/g (fn), 10¹⁷⁴ spores/g (fo), 10¹⁷⁵ spores/g (fp), 10¹⁷⁶ spores/g (fq), 10¹⁷⁷ spores/g (fr), 10¹⁷⁸ spores/g (fs), 10¹⁷⁹ spores/g (ft), 10¹⁸⁰ spores/g (fu), 10¹⁸¹ spores/g (fv), 10¹⁸² spores/g (fw), 10¹⁸³ spores/g (fx), 10¹⁸⁴ spores/g (fy), 10¹⁸⁵ spores/g (fz), 10¹⁸⁶ spores/g (ga), 10¹⁸⁷ spores/g (gb), 10¹⁸⁸ spores/g (gc), 10¹⁸⁹ spores/g (gd), 10¹⁹⁰ spores/g (ge), 10¹⁹¹ spores/g (gf), 10¹⁹² spores/g (gg), 10¹⁹³ spores/g (gh), 10¹⁹⁴ spores/g (gi), 10¹⁹⁵ spores/g (gj), 10¹⁹⁶ spores/g (gk), 10¹⁹⁷ spores/g (gl), 10¹⁹⁸ spores/g (gm), 10¹⁹⁹ spores/g (gn), 10²⁰⁰ spores/g (go), 10²⁰¹ spores/g (gp), 10²⁰² spores/g (gq), 10²⁰³ spores/g (gr), 10²⁰⁴ spores/g (gs), 10²⁰⁵ spores/g (gt), 10²⁰⁶ spores/g (gu), 10²⁰⁷ spores/g (gv), 10²⁰⁸ spores/g (gw), 10²⁰⁹ spores/g (gx), 10²¹⁰ spores/g (gy), 10²¹¹ spores/g (gz), 10²¹² spores/g (ha), 10²¹³ spores/g (hb), 10²¹⁴ spores/g (hc), 10²¹⁵ spores/g (hd), 10²¹⁶ spores/g (he), 10²¹⁷ spores/g (hf), 10²¹⁸ spores/g (hg), 10²¹⁹ spores/g (hh), 10²²⁰ spores/g (hi), 10²²¹ spores/g (hj), 10²²² spores/g (hk), 10²²³ spores/g (hl), 10²²⁴ spores/g (hm), 10²²⁵ spores/g (hn), 10²²⁶ spores/g (ho), 10²²⁷ spores/g (hp), 10²²⁸ spores/g (hq), 10²²⁹ spores/g (hr), 10²³⁰ spores/g (hs), 10²³¹ spores/g (ht), 10²³² spores/g (hu), 10²³³ spores/g (hv

MGLPLGLFCLAVLAASFSKAREEEITPVVSIAYKVLEVPFKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVKTHEFPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCRQPANFSLFLP
SQTSDFWFCQAAANNVQHSALTVVPPGGDQKMEDWQGFLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVVRGRKAAVM

amino acids 1-18

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**AATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGGAAGAAA
 CTAAATGTCAACCGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGTC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTCGAGAGCACCCTCGCCATGTCTTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCTCATCTTTTGCTGCCTCCTCATCCTCCCCCTGCTTCATCTCCTTGCCA
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTCTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTAAATTTATTAATAAGAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTTCTGTACTGATATTTAAATAAAGAGTCTATTTCCTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCQVGGQVDEKTFL
HYDCGNKTVTPVSPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHGPARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTTCGCTGCTAGCTG
 CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
 TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
 GTGTGGCTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
 GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
 TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
 CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAATCAAATTGGGAGGCCAAC
 CCACAGAACAGCATTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
 ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
 CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTGCAGCAAGGGACC
 TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
 CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA



FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACCTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGGCCCC
 AGAACTGCCCTCCGTTTGTCTCGTGCAGTAACCAAGTTACGCAAGGTGGTGTGCACGCCCGCG
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACCTCCATCCCGCAGATTGAGGTGGGGCCCTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCACTG
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGTGGAACCT
 CAACCTGGCCCAACAATAACCTCTCTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTGTGATCTACACCACAACCTTGGAACTGTGATTGTGACATTTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCTGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCAATGGGACAGTGCTCAGCCACGC
 CTCGCCCAACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTCCACAGTGCTGC
 TTTACAGACTGGGGTGACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTCAGACTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA
 CCACGTCCACTGTTTACCAGCCGGCATATACCACCTTACCACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAAGCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAATTCGTAAGCGGCACACAGCAGCGGAGTACAGTC
 ACAGCCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAACACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACACAAACCTTACAAACCAGCAGTATGGGGCCCACTGGACAGAAACAGC
 CTGGGGAACCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGACCA
 TACCAGGACAAGGTACAGGAACTCAAATA**TGACT**CCCCCCCCAAAAAATATATAAAT
 GCAATAGAATGCACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTGA
 TATGCTTATATATAAGTCTATGGGCTGGTAAAAAAAACAGATTATATTAATAATTTAAGA
 CAAAAGTCAAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYLNLMCNIDMPNLTPLVGLLEELEMSGNHFPFIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDNLISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAEINTSNYSFFTVTVTETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQMVSRETPLH
QLYSAAFSKQKLQSAPTCKPALPFGDLPMGYQHLHTQLQYECISFFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWVPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLCEEQHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTGCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCGCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTCTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAAGTGTCTTCTGTGCTCTCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCTGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGTGGAATGGATTCTCT
 AACAACACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGAATCTTTGTTTGGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAAGCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTATTATCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGCAGGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGTGCAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDLRLRVELQRMKISRPLPEVGKYMVFHTRDKGNEVNAERMKLLHQVSR
VVRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTGCGCAGCGGGCTGTGGGCGCGCCGGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCACGCTTCTCCGCTCCGGCCCCCGCAATG
 GCCAGGCGAGTGTGGTCGCGCCTCGGCCGATCCTCTGGCTTGCTGCTCCTGCTCCGCTGGGC
 CCCGCGAGGGTGGCCGAGGCTGTATGAATCAATCTCACCACGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCTGGTGGCCAAGGACAACGGCAGCTTGGCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTTGGCCAGGGGCTTTGTG
 GTCCTCCCCATCACAGATTCTCTGTTGGGGACCTTGTGTACCCAGAACAACCTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTCAACGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGTGAAGCTGCAGGAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTCTGGCGTCTCAAGCCTGAGTGCCTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCAGCGGTACAACCTGACCCACACCTTCAGGACCCCTGGGACTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCATGTGTACACTTATCACTGTGA
 GTTTGGCCTTCATCATGTACATGACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGAGGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTTGCT
 GGAGACTCCATCTGAGTACCTGGAATTTGCTGTGAGAACCACGGGCTGCTCCCGCCCTCT
 ATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAAGGAGGGTTCATT
 TGCGTGGGGCTGTTGGCTGGATCATCCATCCATCTGTACAGTTGACCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCCCT
 CTCATATTGGCACATCTGCTGCCATTGGGGTCTCTCAGTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAGGTCTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTCCGTTGCTGGGATGCACCTGCACTAGAGCTGAAGGGAATTTGACCTCA
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC
 GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTTGGATGGGGGGCAGGACT
 AATACTGAGTGATTGACAGAGTGCTTTATAAAATACACCTTATTTATCGAAACCATCTGTG
 AAAC'TTCACTGAGGAAGAAGCCCTGACGCGGTAGAAGAGGTTGAGTCAAGGCGCGGGCGGG
 TGCTTACGCTGTAAATCCAGCACTTTGGGAGGCCGAGGGGGTGGATCAGGAGATCAGGA
 GATCGAGACCACCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCCGAGTACTCGGGAGGCTGAGGCAGGAGAATG
 GTCCGAACCCGGAGGCGGAGCTTGCAGTGAGGCCAGATGGCGGCCACTGCATCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGFEPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSELLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFISIRAENIISKTHQYHKIQVWPSRIQPAVFAPFCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**GATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCAGAGGCGAAGGAGGCGAGACCCCACCTTCCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTTGTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCCTGGC
 CTGGATCTTCCACC**ATG**TTCTCTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCCAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCCACAGCTTTACAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTCTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGCTGATTCCGTTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTCGCTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGACCATGGTGAAGCCCTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGGCAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACTGCTGTGGGATGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACAC
 AAGGACAGGAGCCGCTCT**TCAG**CCCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCTACTGCTGTGCTTTCCAGACTCCAGGG
 CTCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCCGCCAGCCGACGCGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACCGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTTCTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGGGTTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTCTGGGGCGGCCACCCG
 CTCTCCAGGAAGGCAACAGCTGAGGCACCTGGGCTTGGCTTCCGGCTCAACATCCGCCCCAGC
 CTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGTTACTAAAGGGAGGGGAAGAGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGTACTCCAGGCTAACCTGAACCTCCC
 ATGTGATGCGCGCTTTGTGAATGTGTGCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTTCTTACCTCACAGGCTGTGTGGGATTAAGTGCTGCGGGTGAGTGA
 AGGACACATCACGTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCATGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKSSKALDNTPEFELSDIFYFCRKME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSMIVGNHKDRSRS

FIGURE 168

GCCCTCTGA~~AA~~ACCAGGACTCCAGACCTCTGTTCCCGCCCTACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGG~~ATG~~CGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAG
AAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCGGGAGCTCTACATGAGGCATTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCACTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAAGCAGTGGCCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGCTCGGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGA~~AA~~AGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACTAGTTCCGGACCCAGCCCTCAGACCTCTCCCCAACCCAG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTGATTTGATGGGGACTTCCT
GGGACAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCTCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAATGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCTCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCCGTGTCAGCAGAACTTCTCAAGCCCATCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCTGTGTCTCTGTGTGGTGCCCTT
 CCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
 TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
 CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAASGPKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTHEYDTIPHNTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGGGAA
ACTCCTAACATATGCCCCCATCTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTGCTTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACCCCTTGACAAAT
TTTTTCATGAAATTATTCTCTTCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDL SNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGTCTATTGCT
TGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGTACACAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAP**TAG**TGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTCTTTATGAATTAACTCG
CCCCACCACCCCCTCA

Parameter	Unit	Value
Mean	mm	1.5
Standard deviation	mm	0.5
Minimum	mm	0.5
Maximum	mm	2.5
Range	mm	2.0
Mode	mm	1.0
Median	mm	1.2
Interquartile range	mm	0.8
Skewness		0.5
Kurtosis		1.0
Correlation coefficient		0.8
Regression equation		$y = 0.8x + 0.2$
Adjusted R-squared		0.7
F-statistic		10.0
P-value		0.001
Confidence interval		0.5 to 2.5
Standard error	mm	0.3
Mean square	mm ²	0.2
Sum of squares	mm ²	0.5
Total	mm ²	1.0
Error	mm ²	0.3
Regression	mm ²	0.2
Adjusted	mm ²	0.1
Unadjusted	mm ²	0.2
Mean square	mm ²	0.1
Sum of squares	mm ²	0.3
Total	mm ²	0.5
Error	mm ²	0.2
Regression	mm ²	0.1
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.1
Mean square	mm ²	0.0
Sum of squares	mm ²	0.2
Total	mm ²	0.3
Error	mm ²	0.1
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.1
Total	mm ²	0.2
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0
Unadjusted	mm ²	0.0
Mean square	mm ²	0.0
Sum of squares	mm ²	0.0
Total	mm ²	0.0
Error	mm ²	0.0
Regression	mm ²	0.0
Adjusted	mm ²	0.0

[illegible]

Parameter	Unit	Value	Standard Error	95% CI	P-value
Intercept		1.00	0.00	1.00	0.00
Age	Year	0.02	0.01	-0.01, 0.05	0.15
Gender		0.05	0.02	-0.01, 0.11	0.08
Education	Year	0.01	0.00	0.00, 0.02	0.00
Income	Year	0.01	0.00	0.00, 0.02	0.00
Health		0.05	0.02	-0.01, 0.11	0.08
Marital		0.05	0.02	-0.01, 0.11	0.08
Religion		0.05	0.02	-0.01, 0.11	0.08
Occupation		0.05	0.02	-0.01, 0.11	0.08
Residence		0.05	0.02	-0.01, 0.11	0.08
Time	Year	0.01	0.00	0.00, 0.02	0.00
Time ²	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁵	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁶	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁷	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁸	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁰	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹¹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹²	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹³	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁴	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁵	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁶	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁷	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁸	Year	0.00	0.00	-0.00, 0.00	0.00
Time ¹⁹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁰	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²¹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²²	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²³	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁴	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁵	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁶	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁷	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁸	Year	0.00	0.00	-0.00, 0.00	0.00
Time ²⁹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁰	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³¹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³²	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³³	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁴	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁵	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁶	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁷	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁸	Year	0.00	0.00	-0.00, 0.00	0.00
Time ³⁹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴⁰	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴¹	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴²	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴³	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴⁴	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴⁵	Year	0.00	0.00	-0.00, 0.00	0.00
Time ⁴⁶	Year	0.00	0.00	-0.00, 0.00</	

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGACCTATGCCTTCTATAACAACCTGCCGCCGCTCC
 AGTGTTTCCACAGCCCCCAAAACGGAACCTGGTTTTGGGGTCACTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCGTCGGATGCTGAC
 GCCCCGCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGA
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGGCG
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCTATCCGGAGCGGCGTCG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTC
 CTGGGTCTGTACAACCTTGCAGGACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGATCCTGAGGCTACGAC
 CCCTTCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCCGAGATGAAAGTGGTCCTGG
 CGTTGATGCTGCTGCACCTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTGCGAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEIGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLLASEGS
SRLLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC
AGTGTGGAGAAAACTAGGCAAACACACCCGTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
 GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
 CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
 AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
 CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
 GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
 AGGGGCAGAGGATGAAGTGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
 CAGGGGTTCACTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
 GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT
 AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGTCTTGCAGCAACTCCACGACTGTTTGTA
 CAAGCTCAGGAGGCGAATAAATGTCAAAGTGA

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGGTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAA
 GGGCAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACGAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACCAAGA
 GCCTCCTTGTTCATAACCACAGGTTACCTACAAACCACTGTCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEELKSMRTQQ
AQQEAEELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCGTGTGCGAGAAAGGTCTGGCAGCCAAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAAGTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCAAGTTTCATTGAACCTTACACCACCAGCCAAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAAGTGGGCGCTTTGCTG
 CTGTTTCTCTGTCTCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTTACCTGCTGCATGGCTCGGCTGTCAACCACCTTCA
 ACAGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTCCTCCGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTACCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTGTGTTTCAACCAC
 CCCACATCTCACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTGAGCTTTGGCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCCATTCTGTCACTTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCTTCCCCCTGCCCGCCGTAGATTCTAG
GACATTCGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCCCTGAAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAATTTCTCTAACACTGAAA

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCTGGGAGCCAGGAGCGACGTCA
 CCGCCATGCGCAGGCATCAAGCTTTGATTAGTTTGTCTCTTGGAGGAGCAATCGGACTGATTTTTTGATGCTT
 GGATGTGGCCCTTCCAATATACAAATACTGGCCCTCTTGTCTATTTTTTACATCCCTTCACTCATTTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGGACTTGCCATCTTTC
 TTACAACGGGCATTGTCTGTGCAGCTTTTGGACTCCCTATTGTATTGGCAGACACATCTGATTGAGTGGGA
 GCTTGTGCACTTGTCTCACAGGAACACAGTCATCTTGAACATATACTAGGCTTTTCTTGTGCTCTTGGGA
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAATTAAGTAATTTGTCGAATGGACTTCCTGTCAATT
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTGGGGGTATTTA
 GGTGCTCCCTTCTCACATTTTATTGTAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTAAGAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTACACATTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTTATGTGTTTTCTCTGTAGGTTGATTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATATT
 TAGCTCCATTATTACAAAAAATTATAAAAAAAGTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACCTTATAGACTGTATACTCACTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTAAATGCCATGCCCTCCGTTAAGGGTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGAAGTAAGGTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAATGACATTTGAATTTCCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTTATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTGACTTATTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAAAATATAGTTTAATTAACACTTAGAAGTGTTTACTTACCTGGAATAATTTGCTATGCCGTACATT
 CAGAGTGCCCTTCCCTGCAAGGCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTGATGCA
 TTAACAGTTTAAAGTTTAGACCATGGTAATAGTAGTCTTATCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGCAAGTTTCTGTATACCTCTGAAGTGTGTTGATTTGAGTTTATCATGATAGATCTGTGTTT
 CCTTATAAAGGCATTTGTTGTGTGAGTTAATGCAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 AACTGACCAAAAATTTCCAGTAACCAAGGCATGATCAATTTATAGTGGTCTTTTACATCTAATAATTTATCAGGA
 CTTTTTTTCAAGAGTGGGTATAAAAACATCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATTCAGTATACCTTACATAAAAAATTTTCCGCTCAGCCAAACTCAGTAATCATGACAGCTGTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTGTTCACTGCTTTTACTAAGATGCCATA
 AGCCACAGCTTTTATTGCCCTAATTTAAGCCATGACTTTTAGATATGAGTAGCGGGAAGCAGGACGAATATCG
 GCGTGTGCTGCGAGCCTTCCCATGGAGGCTGAAGTGGCTTGTGATTTAATGTTGAGATTTCAGAGTTCAGAGGAA
 GPGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTCTTGTGCTTGTGATCTACGGAACCT
 TTTTTTGCAGGAAGTGCATCTCTGCT
 TTTTATCCACTTGGCAGACACTTTTCTAACAGCTGCGTATGTTTCTATATAGATTTGATTGATTGATTGATTG
 GTGCTTTGACCTTGATAGCTGTGACATAGTGTCTCTCTGATTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATGAAATATGCACTGATACACATACCATTTCTCTATGGAAGAAAATCTTTGATGATGAACAAATA
 AGATTTTAAATATCTTTTTAAAAAATAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFAHLEWGCALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRLISLHSLCLRNRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRPTYIEPRILNSWKSLSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPSTG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPTATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTVQRRKQKQKQTMHQAAMSAQEYVVDYKPNH
IEGALVINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCAC TGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGCGGACAAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCTCTTCTTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTCCGCCCTAGTGCCTCCTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCGCGACATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGCGTCCCGCGGGGCCGCTACGCTTCCACGGGCCGGGCGCGCTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

[illegible]

FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGGTTCCGGGGGCGTTCCCTCCAGTCAACCCTCCCGCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCTCCAGACCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTCGCAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGCTTCTATACTTGTCTGCACTGAGTCTTTT
 AACCACTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTCTTTTGTGGATTCCGTTGGGATTACT
 TATATAAAGTCCAACGCCCATTTTATTATATTATGAATATGGTGTTCACCTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACTACCTAACCATTTATCTTGGTAACCTGGCTCTTTCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTATCTTATTCGGGAACAAATCTTCTCCTTGGATCAGATGAATATTATGATCCAGTCTT
 GGGAGAGGCGACCAATATGGATCAACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCCGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCATTACAATGAGTCAGTTTCATTGAGATAG
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAGAGCCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCGCTCATGGGGCTGTCTTTTTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTTGGGAACACTCTGAACCTAATCATCACAAGTGATCATGG
 AATGACGCAAGTGCTCTGAGGAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCACTATACCTTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAATCAGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAAATACACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCAGATTTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTGCTTCCAGAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCTCTCCCTGGTAGTGTAAACACAGCAGAAATGACCAAGAGGGGTCATACCCCTATTTCATAGGGGTC
 TCTCTTGGCAGCATTATAGTGATTGTATTTTTTGTAAATTTTCATTAAGCATTAAATTCACAGTCAAAATACCTGC
 CTTACAGATATGCATGCTGAATAGCTCAACATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATTCATAATTATGTCAAGTGTAAAGGTTTCAAAATCTGGGAAACCGATTCCAAACATCTGC
 AGAAACCAATTAAGCAGTTACATATTAGGTATACACACACACACACACACACATACACACACCGGACCAAA
 ATACTTACACCTGCAAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTAATTTGCAGTTGGCGAGATAATGATATATTAGCAACTTTGCACTATGTAAGTACCTTATAT
 ATTCGACTTTAAATTTCTCTCTGATGGGTACTTTAATTTGAAATGCACCTTATGGACAGTTATGTCTTATAAC
 TTGATTGAAATGACAACTTTTTCACCCATGTACAGAACTACTGTTACGCATTGTTCAAACTGAAGGAAAT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTGA
 AAATTAATGTCATAACCTTTGAACCTTGAATTTTGGAGATGTATTCCCAACAGAGATGCAACTGTGGGCAT
 TCTTGTCTTATTTCTTCCAGAGAACGTGGTTTTTCATTATTTTTCCCTCAAAAGAGAGTCAAAATCTGCACAG
 ATTCTTCTAAATATATTGTTCTCTGATAAATATTGTGATTTTCTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACATGAATATATCTTCTCTATATGTCAGCAATGGCCTGAATAGAGAACACAGGCA
 CCTCTCAGCAATGTTTTCTCTTGTGTTGTAATATTGCTCCTTTGAAAATTAATCACTATTAATTACATTAA
 AAATCAATTTGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVSVDFGRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW
ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDKHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNCSFNNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCAG
 GACAGGCCACCTTCGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAAGCGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTTCAAGTCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCAGAGTCACTGGCCAGTTA
 TCACCTTCAAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAAGACAAACC
 AAAATCTATAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFS SHRQV I I I C L V V L D A L L V L A E L I L D L
K I I Q P D K N N Y A A M V F H Y M S I T I L V F F M M E I I F K L F V F R L S S F T T S L R S W M P V V V V S F I L D I
V L L F Q E H Q F E A L G L L I L L R L W R V A R I I N G I I I S V K T R S E R Q L L R L K Q M N V Q L A A K I Q H L E F S
C S E K P L D

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGGCTCGAGGGGCAGTGGAGCACCAGCAGGCCGCCAACAT
gCTCTGTCTGTGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTTCATCCGCTCC
 CAGGAATCTCCACCTACCGCCAGTGGAGCAGAAAATTCTACAGCTGGAGATAGGACCT
 TGATGGCGACTAGACTTTGAAGAATTTCTCATTTATCTCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTTTAGATTTTGGACAAAAGAATGATGGACGATTCAGCGCGCAGGAGCATATG
 CAGTCCCTGCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAG
 CATGGATAAAAACGGCAGCATGACCATCGACTGGAACAGTGGAGAGTACCACCTCCTCC
 ACCCGTGGAAAAACATCCCGAGATCATCCTCTACTGGAAAGCATTCACGATCTTTTATGTG
 GGTGAGAATCTAACGCTCCCGGATGAGTTACAGTGGAGGAGAGCGACGCGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCTCAGAACCTGCACGCGCCCTCG
 ACAGCTCAAGGTGCTCATCAGGTCCATGCCCTCCGCGCAGCAACAACATGGGCATCCTTGGT
 GGCTTCATCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 GCTCTCAAATTTGCCCGCGAATCAGCCATCAATTCATGGCTATGACAGATCAGCGCC
 TTGTTGGTAGTGACCAGGAGACTTCAGGATTCACGAGAGGCTTTGGCAGAGGTCTTTGGCA
 GGGGCTACGCCGAGCAGCATCTACCAATCGAGGTCTGAGAGACCGGATGGCGCTCGG
 GAAGACAGCGCACTACGAGGAATGCTGGACTGCCGAGAGGATCTTGGCCAGAGAGGGGG
 TGCGCGCTCTTCAAAGACTATCTCCCAACATGCTGGGCATCATCCCTCTGCCGCGATC
 GACTTGCAGTCTACGAGACCTCAAAGATGCTGGCTGCAGCATGTGCAGTGAACAGCGC
 GGACCCCGCGCTGTTGTCTCTTGGCCGTGTGGCAGCATCTCCAGTCACTTGGCCAGCTGG
 CCAGTCAACCTTGGCCCTAGTCAGGACCCGATCAGGCCAGACCTCTATTGAGGGCCCT
 CCGGAGGTGACCATGAGCAGCTCTTCAAACATATCTCGGACCGAGGGGGCCCTTGGGCT
 GTACAGGGGCTGGCCCGCAATTCATGAAGGTCACTCCAGCTGTGACATCAGTCACTGG
 TCTACGAGAACCTGAAGATCACCTTGGGCGTGAGTCCGGCTGAAGCGGGAGGGCGGCCG
 CGAGTGGACTCGTGTATCTTGGGCGCAGCTGGGGTGTGCAGCATCTCATTTCTGTAATG
 TGGCAACACTAAGCTGTCTCGAGCCAAGCTGTGAAACCTTAGACGCACCCGACGGGAGGT
 GGGAGAGACTGGCAGGCGCAGGGCTTGTCTGCTGACCCAGCAGACCTCTGTGTGGTTCC
 AGCAGAGACCAAGGACATCTTACGGTCCAGGGTCAAGGCTCCGGGCTCACATGTGTAA
 GGCAGGACATTTTCTGCAGTGCCTGCCAATAGTGAAGCTTGGAGCTTGGAGGCGGCTTAGT
 TCTTCCATTTACCCCTTGCAGCCAGCTGTGTGGCCAGGCCCTGCCCTCTGTGTCTGCCGTG
 ATCTCCCTGTGCCCTTGTGCTGCCCTGCTGTCTGAGGTAAAGTGGGAGGAGGCTACAG
 CCCACATCCCAACCCCTCGTCCAATCCATAATCCATGATGAAAGGTGAGGTCACTGGGCT
 CCCAGGCTGACTTCCCACTACAGCATTGACGCCAAGCTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCCTTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTCAGGGGGCTCGGGCTGCCCTGGCTGCCATGCACAGAAGGCAAGTCTGGGGCTCA
 TGGTGCTCTGAGCTGGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACAACATCACTG
 TCCCACCTGTGGCATGAGGGCAGTGGAGCACCATGTTGAGGGCGAAGGGCAGAGCGTTTGT
 GTGTTCTGGGGAGGGGAAGGAAAGGTGTTGGAGGGCTTAATTTAGGATCTGTTGGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGGAACAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTGCCAAC
 CCAGCAGGGGCGCAGCGGAGCCAGCCCACTTCCACTTGTGTCACTGCTTGGAACTATT
 ATTTTGTATTTTATTTGAACAGAGTTATGTCCTAACATTTTATATAGATTTGTTTATTAATA
 GCTTGTCAATTTTCAAGTTCTTTTATTCATTTTATGTTCACTGATTTGATGTAACCTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTGCACTCAAT
 CTGTCCAGAGAAATTCCTTTGGGACTGGAGGCAGAAAGCGGCCAGAGGCAAGCCGCTG
 GCTCCTTCTTCTTGGCAGGTGGGGGAAGGGCTTGGCCCCAGCCCTTAGGATTTAGGGTTGA
 CTGGGGGCTGGAGAGAGAGGAGGAGAACTCAATAACCTGAAGGTGGAATCCAGTTATTTCT
 CTGCGCTCGCAGGGTTTCTTTATTTCACTCTTTTCTGAAATGTGCAAGGAGTGAAGTGCCTCT
 CACTGTGAATTTGTGTGGGCGGGGCTGGAGGAGGGGCTGGCTCGCTCGCTCCCTCC
 CAGCCTCTGCTGCCCTTGCTTAAACAATGCCGGCCAACTGGCGCACTCAGGTTGCACCTCC
 ATTCACCAGAAATGACTGATGAGGAAATCTTCAATAGGATCAAGAGATCAATGCAAAAAT
 GTTATATATGAACATATAACTGGAGTCTCAAAAAGCAAAATTAAGAAAGAATTGGACGTTAG
 AAGTTGTCTATTTAAGAGCCTCTCAATAAAGTTGTTCAAAGCTGAAAAAATAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKLK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGNI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
 GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
 CAATTGCACTCATCATTTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTGAACCTGACATCAA
 ACTTTCGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAACAAGTGTGTTAAGAGTGATAAG
 TAAATGACAGTGGGAGACAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGCTCGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVWVASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

00000771-112001

FIGURE 209

[illegible]

FIGURE 211

CTTCTGTAGGACAGTCACCCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCAATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTGCGTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTGAGTAACGCCACCTGTGAGTTCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
 TCTTTTCGAAAGTTTGAGTGTGCAAATGTAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGGTCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCCTTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 213

GGCTTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTACTGGCCACCTTCCCAACCCCAAGAGGCCAGCCCC**ATG**GTCCCCGCGCCG
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGGGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCGAG
 CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCAGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCCGTGGCACTGCCAC
 TGC AAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGGCGCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTTGCACCTATCAACAATGTCT
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCAQSTTSTRTTTTFPPTIHLRSSPSLPPASPCPALA
FWKRVIRIGLEDIWNLSVFTMQPIDRNQR

FIGURE 215

CCGCGGTGACCCACGCGCTCCGGGGAGAAAGC**ATGG**CCGGCCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCCGAGGCGACCGCTGAGCGCGGTGACCGCGACTGCGTACTGCAGTGGCGAGAGCA
 GAACCTGCTCTGGGGGGCGCTCTGAATCACTTCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCTT
 CAGTTCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCGCGGCATCGGCCGTGGCCCTGTTTCT
 CAATGGCTGGCGAGCCTGGTGATGCTCTGCGGCTACCGCACCTTCGTGCCAGCCTTCTCCCGCATGTACACA
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGGCTCAGGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCITCCGGGCTCTCTGTGCTCATGCTGACCGTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCTGGCTGTGGAACACCGCGCGCTGCCTCAGCTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGTGCGAGGGGCTGCTCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGCTCTTTTTCAGCTTTCTGGAAATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAGCTGGACT**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGTAGATGATTTTCTCTTTTCAACTCTTGAACATGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGGACGCCCTTACCTCCTGGAGCTGAACCTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTCTCTCCACACAGCCTCCTCCCACTCCCGAGCTG
 CTTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAAGGACACAGGCCCTTAGGGATACAGGGGGTCCC
 CTTCTGTTACCAACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTGTGCTGCTGTGTTGGTGGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGGCCAGGCTGAGTGATAGG
 TGACAGGCGCGCTGAGCATGGCGTGTGGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGAGCGGTTGTG
 CGGGAGAGGAGTGTGGCTTCAAAGTGTGTGTGTGACAGGGGGTGGTGTGTTAGCCTGGGTAGGGGAAAGTGTG
 TGCGCTGCTGCTGGGATGTGAGATGAGTGACTCCGGTGAATGTGCCAGTTGAGAGTTTGGAGCAGGAT
 GAGGAATCCTGTCAACATCAATATCACTTGTGGAGCGCAGCTCTGCCCAAGACGCCACCTGGGCGACAGC
 CAGGACTCTCCATGGCCAGGCTGCTGTGCTATGTTCCCTGTGCTGGTGGCCCTTGGCCGCTCCTGCCAAG
 CTCACAGGCTCCCAACACAGAGTGCCTCCAGAGCAGCCCTCGGAGGACAGAGGAAGGAAAATGGGGATGGC
 TGGGCTCTCTCCATCCTCTTTTCTCCTTGCTTGCATGGCTGGCCTCCCTCCAAAACCTTCCATTCCTCT
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGAGGAGGAGGGCGATTTGAGGGAGAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTTCCCTCCAGAGGCTCTTACTGTTCCAGGCTGCCCCAGGGCAGGCGAGGGCC
 ACATATGCTGTGGCCTGGTAAAGGTGACCCCTGCCATTTACAGCAGCCTGGCATGTTCTTGGCCCAAGG
 AATAGAATGGAGGGAGCTCAGAAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTG
 CTTGCCCTGACCCCTTGTCCCTTTTGGGAGGGGGAGCTATGCTAGGACTCCACCTCAGGAGCTCGGTG
 GCTTGGCTGAGCTCTTTTGATCTGAAAACCTTTTAAGGTGGGAGGTTGGCAGGGAGTGTGCTTATATAATCA
 TTCCAAGCTCAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPPAVVSAFRALLLLMLTVHVSYSLSIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNP EKSSTKETERKETKAE EEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNLSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLA VRVVITLLYDLVTEKMFEEEEAE L TQEMSPEKLQQYRQVHLLPG
 LWEQGWC EITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

[illegible]

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTD
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC



FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCCTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

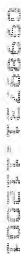


FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNCGCCCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCCACCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCCGCGCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCCCGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCTC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGCGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCGAGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGTCTGTCTCTGTCT
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGTTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCACTAAAGATGTGAGACCCAT
 CAACGTCTCCTCTCATTTGTCCCTCTGTGGGACAAAGTGTCTGGGTGTCTGGGCTGGGGGACAA
 CCAAGAGCCCCAAGTGCACCTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCT**CGA**GTGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCGTACCCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTTG
 GAACAATTTCCAAACTGTCCAGGGCGGGGGTGTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAAAA

FIGURE 226

MATARPPMWWLICALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDDCMHTQFWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIIPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLDLDLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGCAATCCGACCACATTTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCAGGAGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGAC
 TTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGA AAAACTCTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGC GCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAGAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTTACACTTGGTGAATAAGAAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTGTGTTGTTTCACTTACATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCACTTCTTCTTCCATTGACCCATATTTATACCTTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD



FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCGGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTGCGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCCGCCCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGGTCCCGCCCCCTCGGAGACTCCTCTGGTGCT
 CTGGGGGTTTCGCGCGGGCCGGGGACCCGCGGTGCGGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGGCCCGCAGGGCCCGTGGCCGTGGGCGATCTCCCTGGGGCTTACCCTTGAGCCT
 GCTCAGCGTCACTTGGGTGGAGGAGCGGTGCGGCCACGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCCGCGCGCGCAACACCAACGCGCGCGCGCGGCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGCCGGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCTTTCGCC
 CTACCACCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCGATCAGGCAAGGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCCCGCGGGCCCCACCTGGGATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTTGGTGCTGACACCACTTACACCGAGGCGCACGGCCTGGCAGCGCTTAACCTGG
 CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGCG
 GAGAGCCCAACCCCGCGGCTACTGCGACGGAGGCTTTGGGGATGCTGCTGTGCGCGCATGCTG
 CTGCAACAACTGCGCCCCACCTGGAAAGGCTGCCCAACGACGTGCTGAGTGGCGGCCCTGA
 CGAGTGGCTGGTTCGCTGCATTCTCGATGCCACGGGGGTGGGCTGCACTGGTGACCACGAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGGCCAGTCAGGAGGGGGACCCCTCAT
 TTCCGAAGTGGCCGTACCGCCACCCCTGTGCGTGACCCGTGCACATGTACAGCTGCACAA
 AGCTTTCGCGCCGAGCTGAACCTGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAAATACAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGACCATCCCGCCCGGCCCTCCCGCTTTGAGGTTGCTGCGCTGGGACTACTTACGGAGCA
 GCACGCTTTCTCCTGCGCCGATGGCTCACCCGCTGCCACTGCGTGGGGCTGACCCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACACGCTGAGCTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCGCGGCCCTCACTC
 GCGGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGCTACT
 GAGGCCCTACGCTCTCACTGTGCTGCTGCCCTAGCTGCGCGTGAGCGTGACCTGGCCCCTG
 CTTCTTGGAGGCCCTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCCGCGCCAGGCCACGCGCTGGCCCATGCAGATGTCTTCGCACTT
 GTCAGGGCCACGCTGGCAGAGCTGGAGCGGCTTTCCCGGTGCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCGCGCACCCCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC
 TGGACACACTGTTCTCTGCTGGCCGGGCCAGACACGGTGCTCAGCGCTGACTTCTTGAACCGC
 TCCCGCATGCATGCCATCTCCCGCTGGCAGGCTTTCTTCCATGCATTTCCAAGCTTCCA
 CCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCAGCCAGGAGGCTGCTTCTACAACTCCGACTACGTGGCAGCCCGTGGG
 CGCCTCGGCGAGCCCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCCACTTCTCCAGTCTGCATGTGCTCGGGCGGTTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGGCCAGCAGCTGCAGCGCGAGGCTCAGTGAGGACCTGTACCCAGCTGCTCCAGAGG
 GTGCTTGAGGGCCCTCGGCTCCCAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGGAGGG
 CAACAGCACT**TGA**CCCCACCTGTCCCGTGGCCCGTGGCATGGCCACACCCACCCACTT
 CTCCTCCAAAACAGGACCCACTGCCAGCCTCGCTGGGCGAGGCTGGCCGCTAGCCAGACCC
 AAGCTGACCACTTGGTCCCTCTCTGGCTCTGTGGTCCCTGGGCTCTGGACAAGCACTGGG
 GGACGTGCCCCAGAGCCACCCACTTCTCATCCCAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTCTGGGCTGTGGGCTCCACGTATTTATGCAGTACAGCTGCGCTGACGCCAGCCCTGC
 CTCGTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTTGGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCAACATCTCCCTTTTGAGACCTGCCGAAGCTCCCTGCCCTTAATAAACTGGCCA
 AGTGTGGAATAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWEEFPCGPGPPQPGDSELP PRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDEFDFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDDEWLGRCIILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRRSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTALAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAAL TLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTC SARLSEDL
YHRCLOSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCGAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTTCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCCTGAGACCTGCAGCACCATCTGT**CATG**CGGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACCCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCA
AGATCCAG

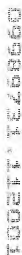


FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGCGCGGCGGCTGGTGCCT
 TGCAGAACCCACGCGACAGCCTGCGGGAGGAACTTGTTCATCACCCCGCTGCCCTTCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG
 TCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCACTTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAAGTACCCTCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTGTATGCCTTC
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCAAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCACTCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCAGTGCCCTTCTGTC
 ATGCCCGAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGTGTAC
 AACACCCACCCATACCGGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGCTGCACCCCACTCCTGGAGATGCTGATTACAGTGCCTG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCCTCAGCGCCCTTGTCGCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACCTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCTCCCACTCT**TGA**TT
 CTTGCCCTTTCAGCAGCTGCAGTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAGTGGCCCTGGACCAGGTCAGGGC
 CTACAGCTGTGTTGTCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTA
 CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGATTGGACAGCACAGAAAAAGATTTCCATCACCAACAGAAAGCTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGATAAAAAAGGCTGTTTCCGTGGAAAAA

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCTTGAGACTTGGAATATGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAAAAGTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGAATCTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLMLVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

100
101
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FIGURE 241

AAACTCAGCACTTGCCGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCAATGAGGTCCTGCCTGTGGAGATCGAGCACCCTGAGCCAAAG
 CGTCCAGTGGTCTTGGCTTGTGGCTGTCTGTGCTTCTTCTTCTCGCTTGGCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCT
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGAGCAGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGAGC
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGAGCCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTTCATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG
 AGCCCCACGACGACAGAAACCAAGACTGAAGGCCCGCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTTCGTGTGGCTCCAGAAACTCTTTCTGCCAACCTCACTCTC
 TTCTGTGACTCCAGACATTCACCCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCAAC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGTGTCTCTGGCCAGCCTCCCGCTGGGAGCCTCGGTGCACTCACTGT
 GCCGTGGTGGGCAACGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCCTCTTGGGAAGGACGTCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGCACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCAACCCAGACTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCAACCACTGGGGCCCTCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACAGGTGAGTGTCTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC
 CCGGAACTGCCAAAGCCAGAACTGAACCGGGGCCAGGGCTGCCATGGTCTCCTTGCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTGGCCATTTCCTGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCGAAGTCTTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAGAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGCTCTATACTGTCTCTG
 TCTTTAAGCTATTTGACAACCTTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCATGGAAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDQTKTTQGNNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKQHRMLAPTGAVSTRTRQKGVTTAVIPPEKEKPPQATPPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
 RYMKNRFLRSKTLDGAAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLI FYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGTCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAAACCTT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT



FIGURE 244

MRGPGHPLLLGLLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACGCGAGTTCTTACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAAACAGGAGCTGAAC TAGA
 ACTATGAGGGGTGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTGTCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
 TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCAAGGGTAGGGGCGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG**ATG**GTGTTTCTGCCCCCTCAAAATGGTCCCTTGC AACCATG
 TCAATTTCTACTTTCCCTCACTGTGGCTCTCTTAACGTGTCCACTCCCTTCATGGTGTACAG
 CACTGAAGCATCTCCAAACAGTAGTGTATGGGACACCAATTTCCCTTGGAAATAAAATACGACTTC
 CTGACTAGCTCATCCAGTTCTATTATGATCTCTTGATCCATGCAACCTTACCACCTGACC
 TTCTGGGGAACCCAGGAATAGAAATACAGCCAGTCAGCCCCACGACCATTATCTCTGCA
 TAGTCACCACTTCGACATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGGCTATCCG
 AAGAACCCTCGAGGTCTCTGGAACACCCCCCTCAGGAGCAAAATGCGACTGCTGGCTCCCGAG
 CCCCCTCTTGTGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAACTAGGATATCTAGCAT
 CAACACAATTTGAACCCCTGCAGCTAGAATGGCCTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACATTTTGATGTCACCTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGCAGCAAGATAAAC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAAATCAAGCAGATTATGC
 ACTGGATGCTCGGGTGACTCTTCTAGAATTTTATGAGGATTATTTACAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGTCTGCTATTCGCCACTTTCAGTCTGGTGCTATGGAAACTGGGGA
 CTGACAACATATAGAGAACTGTGCTCTGTTGTTGATGCAGAAAAGCTTCTGCTCATCAAGTAA
 GCTTGGCATCACAGTCACTGTGGCCCATGAACCTGGCCACAGGTGGTTTGGGAACCTGGTCA
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTGGCCAAATTTATGAGTTTGTG
 TCTGTCAAGTGTGACCATCTGAACTGAAAGTTGGAAGATTATTTCTTTGGCAAAATGTTTGA
 CGCAATGGAGGATAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCTGT
 CTCAGATCCGGGAGATGTTTGTGATGATGTTTCTTATGATAAGGGACCTTGTATTTCTGAATAG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGATGGTATTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAAATACAAAAACGAGGACCTGTGGGATAGTATGCAAGTATTTTGCCCTACAG
 ATGGTGTAAAAGGGATGGATGGCTTTTGTCTAGAACTCAACATTTCACTCTTCACTCTCACAT
 TGGCATCTGACGGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACCC
 AGCAATCCAAATAGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTTGTGCTATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCATTAACAATGCATTTCACTGCTGAGCATTTGGGAAGCTGTCCAT
 TGAAGAGGCCTTGGATTTATCCCTGTACTGAAACATGAAACTGAAATTTATGCCCGTGTGTTT
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATGATGAATGAAGTG
 GAAACTCAATTAAGGCCTTCTCTCATAGGCTGCTAAGGGACCTCATTGATAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACCTACTACTCTCGCCTGTG
 TGCACAACATATCAGCGCTGCGTACAGAGGGCAGAAGGCTATTTGAGAAAGTGAAGGAATCC
 AATGGAACCTTGAGCTCTGCTGCTGTCGACGTGACCTTTGGCAGTGTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTTATAGTAAATATCAGTTTCTCTTGTCCAGTACTGAGAAAA
 GCCAAATTTGAATTTGGCTCTGCAGAACCCAAATAGGAAAACTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATACAAATAAAACTCAGGAGTTTCCACAAATTTCTTACACTCATTTG
 CAGGAACCCAGTAGGATACCACTGGCCTGGCAATTTCTGAGGAAAACTGGAAACAACTTG
 TACAAAACTTTGAACCTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACAAACAAATCAA
 TTCTCCAAGAACACGGCTTTGAAGAGGTAAAGAGTATCTTCACTCTTGAAGAAAAATGG
 TTCTCAGCTCGGTTGTGTCACACAGACAAATGAAACCATTTGAAGAAAACTCGGTTGGATGG
 ATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAGGTGAAAGCTTGAACGTATTTGAAAAA
 TTCTCCCTTGGCCGCTTCTGTTATCTCTAATCACCAACATTTTGTGATGTGATTTTCAA
 ACTAGAGATGGCTGTTTGGCTCCAACTGGAGATACCTTTTCCCTTCACTCATTTTGTGTA
 CTGCTCCCTGTGAAAAAATAGCTGTAGTTTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
 TCTCATCACTGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAAGCTAAACCAAGTGTGTGGT
 TCCCTGCCACAGAAGATAAGTACCTTATTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLIIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEPLQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSYLVLA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWNNDL
 WLNEGFPAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFTITSKNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMEKMRDMNEVETQFKAFLIRLLRLDIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
 RTQNKELQWLLDESFKGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGS
 SSIAHMMVGTNTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTACAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAT
 GAGCATTAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGGTTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCCTTCCTGCT**TAA**CTCTATTACCCACAGATTCTTACCCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATATTATCTACTACCTAACGCA
 AACTGGGAGAGCCTGGAGCATCCGACTTGGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCTTTCA

FIGURE 250

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGGGIFSNLRVQGCMPPQGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGACAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGTGCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCGTGCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCCAACAAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGTGGAAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGTGAAGGGTGGAG
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATG
 AAAGTGTTCCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTGAATTATTACCCAGAATTGCTCTCCATAAAGCTTTGGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCACTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G F P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
TTTATAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCTGTCCCAATCCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCCTGTTCTGT
AACATTCTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCCCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTTCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGTGTGCGCTGCTGTGCG
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTCC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGGTGGTGTGCATCCCCTTGGGGC
 TGCTGTTCTTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTTGTTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCCTTCCTGCGTGGTGGCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCAGG
 GTCCCTCCTCGTCCACCAACCGGAGCCTCCACCTTGCCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGTCCCAGCCTGGGTAACATGGTAAAGCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCAAAA

FIGURE 256

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGTCCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG



FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAAGCTTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCGTGTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTTACCATTGCAGAAGCTTCATTCAAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCCCTCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTT¹GAGACATCCTT
GAGAGAAGGCCACAGCATTAAGAGCATGCGCTGCTTGGTGTTTTGCAGG²GATGATGGTGGCCCTT
CGAGGAGCTTCTGCATTGCTGTGTTCTGTTCTTCGAGCTTTTCTGCCCCGGCCGATGTAC
CCAGGACGCCAGCATGTGTCATTACATCTACACGGCITTTCGAGTCTTGGAGCAGGGCTGG
AAAATGTATCCCAAGCAACGAGGGCATATCTCAAGAATTTCAAAGATTTCTCAAAAATAATA
TCTGTCTAGCTGGGAAGATGTGCAGACTCACAAGTACAGATGACAAAGATGCGAGTGGGTAACTT
GGCATGCGAGGTTGAACGCTGCCAACGGGAGATTGACTACATACATACCTTCGAGAGGCT
ACAGTGTCATCGTATCAGAGGACAAGACATGCGCAGAAATGTGCTCCAAGAAGCTGAAGAA
GAGAAAAGATCGCGCATCTGCTGAATCGAAGTGTGACAACTGCTGATGGGCATAAAGTCT
TTTGAAAATAGTGAAGAAGATGATGACACACATGGCTCTTGATGAAGAATGCTGTCTATAT
ACTCTCCAAAGGTGTACTATTATAATTTGGATGTGACGAAAAACAATCTGTTTGGGAATTTGCAAC
ATACGGGCATTCTAGGGAGATAACCAAGCCAGCTCCCCTGAAGCAAACTCTAACACTTTC
CTGGCAGGGAACAGGCCAAGTGTACTACAAGGTTTTCTTATTTTTCTATAACCAAGCAACT
CTAATGAGATAATCAAAATAAACCTGCAGAAAGGAGCTTGGGAAGATCGAATGCTGCTCCA
GGAGGCTTAGCCCGAGCATTTGGTTTACCAGACTCCCCTCAACTTACATTGACCTGGCTGTG
GGATGAGCATGGGCTCTGGGCCATCACTCTGGGCCAGGCCACCATAGGCCAATTTGGTGTCTCA
CAAGATTTGAGCCGGGCACATGGGAAGTGAGCACTTATGGGATACCCCTACGAGAAGCCAG
GATGCTGAAGCCCTATTCTCTTGTGTGGGTTCTCTATGTGTGCTACAGTACTGGGGGCCA
GGGCCCTCATCGCATCACTGCATCTATGATTCACCTGGGCATATCAGTGAGGAGACATTCG
CCAACCTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCACAGAT
AAGCAGCTCTATGCTCGGAATGAAGGAAACAGATCAATTTACAACCTCCAGACAAGAGAAA
GCTGCCCTCGAAG³TAATGTCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCT
TACAGGACAGCTGAGGCTATAGCCCTTACAATATAGTATCCCTCTAATCACACAGGAAG
AGTGTTGAGAAGTGGAAATACGTATGCTCTTTTCCAAATGTCACTGCTTTAGGTATCTTCT
CAAGAGCTTAGATGAGGACATATCATCAGGAAGTTTCAACATGTCCATTACTCCCCAAAC
CTCTCGGCTCTCAAGGATGACCACTTCTGATACGCTACTTCAAGCCTTTTGTTTATTCT
GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCAACTTAGAGTTGTATGCGAGC
CCCTTAATATCCAACTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
CAATGTCTATTGATATTCCCATTTTCTAGTCCCACTAAAATACTATTAATATTCTTT
CTTTCTTTTCTTTTCTTTTGGACAAAGCTCTCATATGTTGCCAGGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCTCTCGCTCGCTCAGCTCTCAAGTACTGGGATACAGGATGTGCCAC
CACACTGCTGCTTAAATACTATTCTTATTGAGGTTTAACTCTATTTTCCCTAGGCCCTGTC
TCTTCACTAAGCTTGGTAGATGTAATATAAAGTGAAATATTAACATTTGAATATCGCTTT
CCAGGTGTGGAGTGTTCGACATCAITGAATTTCTGTTTCACTTTTGTGAACACTGCACAA
TCTTTACAGCTGTCACTCTAGAGTTTAGTGAGTAAACAACATTAAGAATGAAGATACAGC
TAGAAAAATACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
TGTTCACTCACTTCTATTAGTACAATGGCTCATGTTTCAGCCTTAAAAATATGATCTGTCCCT
TTTAGCCAGTTTTCATGTCTGCACAGCACTTTCATAGAGCCCTTTCAATGATATTTCTCC
AGAAAACCAAGTCTAAGGCTGAGGACCCCACTTAGCCTCTCTTGTCTTGTCTGCTCTGT
TTCTCTCTTTCTGCTTTTAAATTCAAATAAGTGACACTGAGCAAAAAAATAAAAAA

MMVVALRGASALLVFLAAFLPPFQCTQDPAMVHYIYQRFVLEQGGLKCTQATRAYIQEFQE
FSKNISVMLGRCTYTTEYSKSAVGNLALRVERAQREIDYIQYLRADCEIVSEDKTLAEMLL
QEAEEEKKIRTLNLASCDNMLMGIKSLKIVKMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAAPRKQILTLWSQGTGQVIYKGLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTIYIDLAVGEHLGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFALCYGVVYSTTGQDGHRTICIDPLGTISEEDLPLNFFPKRPRSHSMIH
YNPRDKOLYAWNCGNOIYKLOTKRKLPLK

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVIALALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACCTGTGTCTGACTGTGCTGTGATCACAGGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGTGCTCCATGGACTTGAAGAACATCAATTTT**TAG**GCGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTA CACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAGGTTGGCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCTCCCTCCCTCCCTCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTCATCTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCACAGCTTTCCATTAAAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGCAATTAGGTTGTTTCTTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGEECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGCGCAGAAGGGAGGCACTTGAGAAATGTCCTTTC
 CTCCAGGACCCAAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCCTGGCATTGCTGCTTGCCAAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTCATGGGATGTATT
 GTTTCCACTCGTGCCCTAAGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 CTCTACTAAAAATACAAAAATACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTEKEPR
 TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
 QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVVYNFFRAWNGGFSGNLEGEFILGGVFV
 VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCC**ATG**GGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCATC**TAG**GTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCGAATAACATTTGGGT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAAATACACATATTAGTATTACCTTAGTGAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAAATCAGTAAGTATGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCGCTGCTGCACCACTCAAACTACTTCTCTTATTAAAGCTGAATTAATATGGCTTTGAAGATA
 ATGGTCATTGTTATAGATCTTAGTCTGCCAGAGATGAAAAAATAATTTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACTCTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATCTCTGAGAATTTGAAGAAAAATCCTCAGTACAAAGGCCAAAACATG
 AAAACCCATAAACATGCTGATGTTATAGTTGCACCACTTACCTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTTCCACAGAAATGTGGAGAGAAAAGCGCAATACATTTCACTCACCCCTGACCT
 CTACTTTGGAAAAAACAATAATGAATATGGACCAAGCAAGTACAGCCTTTCTACCGTGCTAAG
 CTCACCTCCGGTGGGGAGTGTTTATGATGAGTACAATGCAAGTATCTCTGCTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATACAGAAATGATTTCTACAACAAAACCTGTATG
 AAAAGATTTGCTAAATCTTTTCTCATAAAGTACAAAACGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTTGATTTCTGTTTGTATTTTGTAAACGAAAAAGCCATATAGCAATTTGAGGATT
 CCTACAAAACATAAAAGTGCATTTTCAACCACTCTCTCCACTGCTCTCTATTGCTCAAGATC
 TTAATAAACACCATACCCATGGTGACCACTTCTGATAGTCTGGAAGCATGGGGGGTAAAGACCCCT
 AGTCAAAAGAAATTTGTGCTTAGTTCTTGTGATAGTCTGGAAGCATGGGGGGTAAAGACCCCT
 AAATCCGAATGATCACTCAAGCAGCAAACTTTCTCTGCTGACAGACTGTTGAAAATGGATCCTGGG
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAATAAAGCATTAACCAATAAAAAGC
 AGTGAATGAAAGAAACACACTCTGCGCAGGATTTCTACATATCCTCTGGGAGGAATCCCAT
 TGCTCTCTGGAATTAATAATGCAATTTCAAGGATTTGGAGAGCTACATCCCACTCGATGGAT
 CGAAGTACTGCTGCTGATGTTGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGT
 AAAACAAGTGGGGCCATTGTTTATTTATGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGTGAAGCAAGATAACAGGAGGAAGTCAATTTTATGTTTACATGAAGCTCAACAATG
 GCTCTATTGATGCTTTTGGGGCTCTTACATCAGGAATACTGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAAAGTAAAGGATTAACACTGAATAGTAATGCCGTGATGAACGACATGCTATAAT
 TGAATAGTACAGTGGGAAGGACAGCTTCTTTCTCATACATGAAGACAGTCTGCCCTCCAGTA
 TTTCTCTCTGGATCCAGTTCGAACAATAATGAAAAATTTCAAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATCCAGGAACCTGCAAAAGGTGGGCACTTGGGCATACAAATTTCAAGC
 CAAGCGAACCAGAAACATTTAACTATTACATAACTCTCGAGCAACAAATCTTCTGTGTC
 CTCCATACAGTGAATGCTAAAAATGAATAAGGACGTAAACAGTTTCCCAAGCCCAATGATT
 GTTTACGCAGAAATTTCAAGGATATGTAACCTGTTCTTGGAGCAATGTGACTGCTTTTAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATTAATGGTGAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGTTCTGGGCTCATGGAGGAGCAACACTGCCAGGCTAAATTTACGGCTCCACT
 CAATAGAGCCGCTACATACCAGGCTGGGTAGTGAAACGGGGAATTAAGCAAAACCCGCCAA
 GACCTGAATATTGATAGGATACTCAGACCACCTTGGAGGATTTCAGCGCAACAGCATCCGGA
 GGTCATTTTGGTATCAAGCTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTCA
 AATCACAGACCTTTGATGCCACAGTTCATGAGGATAAGATTATTTTACATGGACAGCAGCAG
 GAGATAATTTTATGTTTGAAGGTTCAACGTATATCATAGAATAAGTGAAGTATTTCTT
 GATCTAAGAGCAGATTTTGTATGATGCTCTCAAGTAAATACTACTGATCTGCTCACCAGGA
 GGCAACTCCAAGGAAGCTTTGCAATTTAAACCAGAAAAATCTCAGAAGAAAAATGCAACCC
 ACATATTATTGCCATTTAAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACTT
 GCACAAGTAATTTGTTTATTTCCCTCAAGCAATCTGATGACATTGATCCTTACACTCTCT
 TACTCTCTACTCTCTCTCTGATAAAAGTCATATTTCTGGAGTTAATATTTCTACCTGTGAT
 TGCTCTGATTTGGGTCTGTTGTATTTGTTAACTTTATTTAACTACACCATTT**GCA**ACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAACAAATGTAAAT
 AAAGATATTTCTGAAATTTAAATTCATCCATGTGTGATCATATAAATCATAAAAATAAT
 TTAAGATCTCGGAAAAAGGATACTTTGATTAATAAAAAACACTCATGATATGTAAAAATCT
 CAAGATTAATAATTAATTTTCAATTTATTTTATTTTATTTATGATGCAACAGTCTTTCTGAAAT
 AAAGATCTTTTCTACTGATACCTGGTTGATATATTTATTTATGATGCAACAGTCTTTCTGAAAT
 GATATTTCAAATTTGCATCAAGAAATTAATAATCATCTGATGATGTCATAAATCAAGATTA
 GGAGAGCAAAATAACAACTTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLITITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDDGVYSRYFTAYTENGYSKLVRAHG
 GANTARLKLRLPPLNRAAYIPGWVNVGEIEANPPREIDEDTQTTEDEFSTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIILTWTAPGDNFDVGVQRYIIRISASILDRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
 GGCAGGGGTGACAAACCTGTGATCTTTTGTATCTCGTGTGGGTGCTCTTCTATTTCAAGGAAAG
 AGCCAAAGGTAATTTGACCAGAGGAGCAATGATGAGCCACCTCTCTAACCTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCACTCAACCAGCAAGCGGGCTCCTTCCGGCTTAACTT
 GTGGTTGGAGGAGAACCTTTGTGGGGTGCCTTCTCTTAGCAGTGTCTCAGAAGTGTACTTGCCTGA
 GGGTGACCAAGAAAGAAAGAGGTCCCCTCTGTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGTGAATCTTTGGAGATTTCACTTCAGTCACTTCTGCTGCAAGATCACTCTTTAAAA
 GTAGAGAAGCTGCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGGCCCAAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTTCCGTGGGG
 GCCCGGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGGTTCCGC
 GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTGTGCTGGTCTCCTCTGCTGTGCTATCTGT
 CCTGTACATGTTGGCCTGCACCCCAAAGGCTGACGAGGAGCAGCTGGCACTCCCAAGGGCCACAGC
 CCCACGGGAGAGGAGGCTACAGGCCGTCTTCAGAGCTGGAGAGCAGCAGCAGCACTACGTGA
 GCAGCTGAAGCGCCAGATCCACAGCTCAGGAGGAGCTGACAGAGAGTGTGACAGCTCAGGAA
 TGGCAGTACCAAGCCAGCATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCAGAGAAAACCCAG
 GCGCACTCTTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGTGAATGCTGGCCTCAAGCTGG
 CCACAGAGTATGACGAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
 CCTTACCCGCCACCCCGAGGAGAAAGCTGTGAGGAGGACAAGCGGGATGAGTTGGTGAAGCCATT
 GAATCAGCCTTTGGAGACCTTGAACAATCTTGCAGAGAACAGCCCCAATCAGCGTCTCTTACACGGCTT
 CTGATTTTCATAGAAGGATCTACCCGAACAGAAAGGACAAAGGGACATTTGATGAGCTACCTTCAA
 AGGGGACCAACAAACGAATTTCAAACGGCTCATCTTATTTCGACCATTCAGGCCCATCATGAAAGTG
 AAAAAAGAGAGCTACACATGGCCCAACAGCTTATCAATGTTATGCTGCCTCTCAGAAAAGGGTGG
 ACAAGTCTCCGGCAGTTTCATGCGAATTTTCAGGGAGATGTGCTATGAGCAGGATGGGAGAGTCCATCT
 CACTGTGTTTACCTTTGGGAAAGAAATAATGAGTCAAGGAATATCTGCAAAAACCTCCAA
 GCTGCACATCTCAGCAATTTACTCTCAGCTGAATGAGGAATTTCTCGGGAAGGAGCACTTG
 ATGTTGGAGGCCCTCTCGAAGGGAAGCAAGCTCTCTCTTTCTGTGATGTGGACATCACTT
 CACATCTGAATTCCTCAATAGTGTAGGCTGAATACACAGCCAGGGAAGAGTATTTTATCCAGTT
 CTTTTAGTCAGTACAATCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGC
 AGCTGGCTATAAAGAAAGCAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCAATCTCG
 GTCAGACTTCATCAATATAGTGGGTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAGATGTGCATAGCTCCAA
 GGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTGGTGTTCAGGACGAGATAGAGGCTCAC
 CTTCCGAAACAGAAACAGAAGACAAGTAGCAAAAAAACA**TGA**ACTCCCAGAGAAGAGTTTGTGGGAGA
 CACTTTTTCTTCTTGTGCAATTACTGAAAGTGGCTGCAACAGAGAAGAAAGCTTCCATAAAGGACG
 ACAAAAGAAATTTGAGCTGATGGGTGAGAGATGAGAAAGCCCTCGATTTCTCTGTTGGGCTTTTAC
 AACAGAAATCAAACTGCTGCTTGTGCTGCAAAAGTAAACCACTTCCGCTGTGAAGTGTGACAA
 AAGCAGCAATGCTTTGTGAGATATAAGCCTAATGGTGTGGAGTTTGTAGTGTGTTACAATACACT
 GAGACCTGTTGTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTGTGAAAAATTCAT
 TAGCATGAAGGCGAAGCATCTTCTCTCATATGAATGAGCCTATCAGCAGGGCTGATGTTTCTAGG
 AATGCTAAAAATCATGAAAGCGAGGAGAGGATAGGCTTATTATGATACAGTGAATACATTAAGTA
 AATTAAGATGGACCAAGAAAGAAAGAAACCAATAAATATCGTGCATATTTTCCCCAAGATTAAACA
 AAAATAATCTGCTTATCTTTTGGTGTCTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAAT
 GCATCTTTTTTCCCTTGTGAGTTTATAGTCTGCTTTATTTAATACCACTTTTGAAGAGCTTACAAGAGA
 GCACAAGTTGGCCATCATTTTTATATTTTTAAGAGATACCTTTGAGATGCAATATGAGAAGCTTTCA
 GCTTCAAAGCATCAAATTTGATGCCATATCCAAGGACATGCCAAATGCTGATCTGTCAGGCATGAAT
 GTCAGGCATTCAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACACATATCTTCTCTGAA
 GAGTATTTTCAAGAGAGCACTGACACTGACCTGCAGAGAAAGAAATGACCTCTTCTGCTTACGAA
 AAGCAACTCTTCAGCTGGTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 GAGTATGGGACCGCTTCTTACCTGTTTAAATAAACCAAGATATACCGTGTGAACCAACAATCTCT
 TTTCAAACAGGGTGTCTTCTCGGCTTCTGGCTTCCATAAGAAGAAATGGAAGAAAATATATATAT
 ATATATATATATTTGAAAGACATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTACAT
 GTTTCCACCCAGGCGAGTGAAGTAACTGAATATTTTTTAAATTAAGAGTCTTACTCAATCA
 CCAAGATGCTTCTGAAATATGCAATTTTATACCATTTCAAACATTTTTTAAAAATAAATACAGTTA
 ACATAGAGTGGTTTTCTTATCATCTGTAATAATATTAGCCAGCAGCATGCATGAGCTAATTTATCT
 CTGTGAGTCTGCTTCTGTTTGTCTCACAGTAACTCATTTTAAAAGCTTCAAGAACATTTCAAGC
 TGTGTTGTGTAAAAATGCAATGATTGATTGATCTGGTAGTTTATGAATTTAATTAACACAC
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGA

MMVMVRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTKGEQYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEEKVPRKDKRDELVEATES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKEHFRLILFRPFSP
MKVKNEKLNMANTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFPYPLVFSQYNPGIYIGHDAVPPLEQQVLVIKKTGFWRDFGFGMTCQYRSDFI
NIGGDFLDIKGWGGEDVHLRYKYLHNSNLIVVRTVPRGLFHLWHEKRCMDLTPEQYKMCQS
KAMNEASHGOLMLVFHIEAHLRKKOKOKTSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAATGCTTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCCTCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAC
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAACATTTGTTTTCTGTGTGACTGCTGAGCATCTTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTCTTTTGTAAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACGAC
 TCAAAATATTCTAAAAATTTTTTCTGCAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCATATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCTCT**CATG**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCGAAGACAA
 GAACCCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCACTTCTGAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTCTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATCAAAGTGTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAATATGAGACACATCTTGTCTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTGCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILWKLQFDDNGTYTCQ
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLETD

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTCTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGCTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTGTCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCACCCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGCTCCCT
GAGATGGAATCAGCTTGAGTCTCTGCAATTGGTCACAACTATTATGCTTCCTGTGATTTC
ATCCAACTACTTACCTTGCCCTACGATATCCCTTCTATCTCTAATCAGTTTATTTTCTCAA
ATAAAAAATAACTATGCGACACATAAAAAA

FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
 TAASTTARKDIPVL PKWVGDL PNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTTGGGTGAGGACGACAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACACAGGCTGG
ATTTGCCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTCGGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWSVRDAEDAHRLQFFVTERTLGKVQRWSGVHTQTGGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ



FIGURE 285

GT**CATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
 GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
 CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCC**TGA**ATCTGCCTGGATGGAATGAG
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQLRLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCAGACAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAAATAGGCTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAAATCTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCATGCTGGCAATAATACC
 TTGTGAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTTCATTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGAAAATTGCATACGCTGTGTCAATT
 TTTTATCTGCTAGTGCTATTCTGCTTGTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AAGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCCGAGCCCC
 TCAGAACCAGACCCAGAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTACAGCCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGCAACCTGGAAC
 TGGCCTCTCACAGGGGAGTTTGGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAAGAGGTATTTTGATACAGAGTGCGTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAAATCCCAAAC
 GTTTGATGAGATTAACTCTGAAACCAAATTAATTTCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCTGTCTTACCAGAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAAACATGAAAACCGAGAAACATGGAAGTTTCTTCCGAAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAGAATCTTCTCACCCTTTG
 CTGACCTTAGTGAACTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGCAGAAAATTAC
 TGCTTATTCATGCCTCCTGTCTCAAAAGTGGACCGGCCATTTTCATTTTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**TTCAGG
 ACATGCATAAGCACTTCTGTCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTGTCTTAACTAGTTTGAAGGTGTTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCTGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCTACTCAGAACTGATCAGAATGGCATGC
 TGCTTAAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTGGACCATGGT
 TGACCATGGTTAACTGAGCTGCAGAAAGCAAACCATGGATGAGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATG**AG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCCAAA
AAAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTGTATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGTGGACCTGGTGGCCAGCGTGATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAAACAGCATCTTATTACTCACCTATGGCCAGCGGAATTCACTGCGGGATT
 TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTGTATTGGAGTGGATATGGAATCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEAS PQQCGDFS GFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCGCGCGCGGCTGCGCAGAGGAGCGGCTCTCGCGCGCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGAAGCTCGGCGCGCGAGGTGCTTGGGCGG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATCTCT
 CTTTTTGA AAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTGA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACTCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCATCTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACCTCAGTGCTTTTCAGAGCTGGATATATCTTAATTAATGACCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLGLQLVLLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTMHSEAKKGSKFDTGSFVGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCACGCGATGCGCAGCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCGGTGCTGCTGCTGGC
 GCAGCTGTCAGACGCCGCCAAGAATTTGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT
 CATGTTGTGGAGCCCATGCCGTGTGCGGGGCCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTTGGGGATCACCAGCCTTT
 TGCAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGCTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCCTCAGCTAAATTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGTGATTTACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTAAAGACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTACGGGTTTTG
 TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCACTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGTTAAACGGGAT
 CTAATAATGCCTGTTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGTCGTGGTGAGAGCAGCTGTTGAGCTCCAATATGTGCAGCTTGAAC
 AGGGTGGGTTGTGGGTGCCTCTTCTGAAAGGCTAACCATTATGGATAACTGGCTTTTT
 TCTTCTATGTCCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCAA

MATLWGGLLRGLSLLSLSCSLSVLLLAQLSDAAKNFEDVRCCKICPPYKENSGLHIYNKNIS
 QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII IYLSILGLLLLYMVYLT
 VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKEVYAQQRWKLQVQE
 RKSVFDRHVVL

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
 CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCTGTCCCGCGGAAGCGG
 CAGGAGCCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
 CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
 CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
 ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
 TAAGGTAAGTAGAATCATCCTAATCATATTACATCA**TGA**AAATCTAATATGGCGATAAAAA
 TCATTGTCTACATTAATACTTCTTATAGTTCATAAAATATTTCAAATCCATCATCTCTTAA
 AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
 TTTACTCAATGTTTAAAGTGTTTGGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
 GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

302/330

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIPIYGFIFLYILYILFKVSRILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTC
 TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTCAGTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG
 GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTTCCGAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCGACCTTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAACAACATTTACTCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAACAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGTCCGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCTCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWG HFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPII VREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKS GGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACCTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTAAAACCTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGCGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGACACAAAC
TGGAGATATTTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCCGGAGAA
GCCCCGGCAAACGCAAGGCTAAGGAGACCAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAATTTATTTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTTGCGGTGCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTACATTTACCAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKSGKTSCDKNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGAAAGGGGACGTTTTCAATAGGAGGCAAACCTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCCACGGGTGGTAACTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG
 CGCGCTCCGGGCGCCTGCCGCTTTGGGGGTGTCTCTCCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGCTGTCTGG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGTCTCCTCATCCTG
 CTGTCAAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTACCAAACCTGTTCTGCCGCGAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCTGTCTGCGCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCAATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKSLCQQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPPSPPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
 RQDPQLKGIVTRLYCRQGYLQMHPDGALDGTGKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPFVNKSKTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAGAGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGACGCTTTCTCCTGGAAACCGAACGCAATGGATAAAGTGTATGTGCGACAGGAGCATTCAAGAATG
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACAGGAGCATTCAAGAATG
 AAATAAACCCAGAGTTAGACCCCGGGGGTGGTGGTCTGACATAAATAAATATCTTAAAGCAGCTGTTCCC
 CTCGCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAAAGAAAAGTATGTTCAATT
 TTCTCTATAAAGGAGAAAGTGAACCAAGGAGATATTTTTGGAATGAAAAGTTTGGGCTTTTTTAGTAAAGTAA
 AGAAGTGGTGGTGGTGGTTTTCTTTCTTTTGAATTTCCCAAGAGGAGAGAAATTAATAATACATCTGC
 AAGAAAATTTAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAAATGACGGATAATGCAAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTATCTCTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAATAACAAGTGTGAATTCGAAGGACCAACACAGATAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCTGACGACCAAGCTTCAGCAAGGTGATTTGTGTTCCGAAAAACCTCGGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACAGGCTGCTGAACCTCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGACCTTGA
 GCCTTGGAAATCTACAGTTGAGTAGGAACCATATCAGAACCATTGAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTCTTGACAACTCGTCTTACTACCATCCGGAATGGAGCTTTGTATACTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAAATCCTTCTTT
 CGCGGACTAGACTTAGGGGAATTTGAAAAGACTTTCATACATCTCAGAAGGTGCTTTGAAGGTCTGTCCAAAT
 TGAGGTATTTGAACCTTGGCACTGTCGAACCTTCGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGTGACCTTCAAAAACT
 GTGGATGATACAGTCCGACATTCAAGTGAATGAACGGAATGCCTTTGACAACTTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACACCCCTTGGAACTGTAACCTGTGACATACTGTGGCTCAGTGGTGATATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGTAACTCTCCCACTCTAAAGGGGAGGTACATTGGAGAGCTCGACACAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTCGACACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCTAAATGGAACAGTCAATGACACA
 TGGGGCTACAAAGTGCAGATAGCTGTGCTCAGTGAATGGTACGTAAATTTCAAAATGTAACCTGTCGAAGATA
 CAGGCATGTACACATGTATGTTGAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCTCCAGTGGTGCAGTGGGAGACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTACCATCCCACTGATGATATACAACTGAGTGAAGTGCAGGAAT
 GATGAGGTCATGAAGACTACCAAAATCATATTGGGTGTTTTGTGCCATCACACTCATGGCTGCAGTATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGAGACACACCCATGGAAAGCCACTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCAACACAACAGTTAAACAAATAAATTCATAACA
 CAGTTGAGTGCATGAACCGTTATTGATCCGAATGAACCTTAAAGACAAGTGTACAGAGACTCAAACTCAAACA
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAACAAGAAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGCAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLVLLALQLLVVAGLVRAQTCPSPVSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNLTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYNLNLAMCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTDNNVGTPVVDWETNVTTSITPQ
STRSTKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCGCCCCGGCACAT
GGCTGCAGCCACCTCTCGCGCGACCCAGGAGCGCGCGCCCGAGCTCGCCCGAGGTCGCTCGGA
GGCGCCGGCGCGCCCGGAGGACCAAGAGCAACTGAGCGGGGAAGCGCCCGCTCGGGGATCT
GGGAT**GTG**TCCCTCTCCTCTTCTCCTCTTGCTAAGTTCTCTACTATGTGTGGAACCTTGGGGACATCA
CACTGAGATCAAGAGAGTGGCAGGAGAAAGTCTACTTGGCCCTGCCACCATCAACTGGGGC
TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAAGGAAACCAAAAA
GTGGTGATCACTTACTCCAGTCTGCTATGTCTACAAATACTTGACTGAGGAACAAGAGGGCC
AGTGGCCCTTTGTCTTCCAATTCTCTGCGAGGAGATGCCTCCTTCAGATTTGAACCTCTGAAG
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGTGTGGAGCCAT
GTCTATCTTAAAGTCTTAGTGAGACCATCAAGCCAAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGAAGCTGAGCTTTGCGATGTGAGTCACTCCTTGCGACAGGCCATTTGTGTAAT
ACTGGCAGCGGAATCCGAGAGAAGAGGGAGAGGATGAAGCTCTGCCTCCCAATCTAGGATT
GACTACAAACCCCTGGACAGAGTCTGGTACGAGTATTACCATGTCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGGTGGCGAGTAACTGTACAGT
ATGTACAAGAATCTCGGATCGGTTCTGCAGGAGCAGTGCAGCGATAGTGGCTGGAGCCCTGTGA
ATTTTCTCTTGTGTGTGCTGCTAATCCGAAGGAAGAACAAAGAAATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCTGAGCTCTCGGAGCTACGCTCTGTGTTCTCTCTCCACTCGCTCCACAGAAAT
AGTGCTCAGGCAGGCCAGCGGACATGTCTCAACTGACGACAGCCCAAGCGAGGCTGTGCCAT
CCAGGCATACAGCCTGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATT
CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGGACAGCTCTCCAA
ACGGT**CTGA**ATTACAATTGGAATGTGACTCCACGCTTTCCTAGAGTAGAGGTCCTTTGGACTC
TTCTCGTCACTTGAGCTCAAGTCAAGCAGGCCATCAACCAAGATGAGAGTCACTTAAGTAGCA
GTGACAGTTGCAGGAAACGAGATTTCAGATGACATTTTCTTATACATAACCAACAAAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCGAGGATCCAAATCTATTTTGTACACAGGACCTGTGGTGAGAGGTTGGGGAAGAGTG
AGGTAATATACCTAAACTTTTAATGTGGGATATTTGTATCAGTGGCTTGATATCAAAATT
TTCAAGAGGAATGGGATGCTGTTGTAAATTTTCTGATGCATTTCTGCAAACTTATTGGATT
ATTAGTTATTACAGAGCTCAAGCAAGCAACCAACGCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAATCCAAAAGAGGAAACATGTGCTCTTATTCTGACTTAAC
TTCATTGTCTATAAGGTTTGGATATTAAATTCAAGGGAGGTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTGTTATTGAGCCAAAATAAC
TATGAAAGGAGACAAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCACTCTTCATGATGTT
ATGAGGATTGTTGACAACAACTAGAATAATATATGAGCAACTTGTGATTGTTTCCCTCAAAAT
CAGATGCCTCTAAGGACTTTCTCGTAGATATTTCTGGAAGGAGAAATAACAACATGTCAAT
TATCAAGCTCCTTAGAAGAAATCTCTTAGAGAAAAAGGATCTAGAAGATCTGAAGATTA
CCCAACATACCAATTATAGTCTCTTCTCTGAAAAATGTGAACACGAATTCGAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTCTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAATAACGACAGGTGGAGGTGCAGTGAGCCGAGATTATGCC
ATTGACCTCCAGCTGGGTGACAGAGCGGAGCTCCGCTCTC

FIGURE 316

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCQESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

[illegible]

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSL SITPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKVHHDIREDVPPPKSRTSTARSYIGSNHSSLGMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCCTCAGGCAGCCAGCC
 CTCAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAG**ATGA**AATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCGAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTTTCAAAAA
 CCACCACAAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACT
 TTGTTCTCATCGTGTCAAACTGCAACCAGTCAAGAAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGGAAGTGGACATTCTTCTGACCTGGATGCGAAAATTTACAAAGC
 TCT**GA**ATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTCCCTGTGTCATTTCA
 AACAGTCTCCCTTCCATATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPELLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCCTCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCTCTACA
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTCTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAAAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
 GGTTCATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGCCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGGATCACACTATTTGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAACAGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATCACTTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCGGATGACCCCGGCCCGGCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYL CMDFRGNIFGSHYFDPENCRFQHQTLLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAATTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCGGCCCATTTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGCCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTACAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTGACACCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAGAGACACTCACATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCGCTCAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGAGCATCAGAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTGTC
 ACAGCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGTGGGTGACAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCCTCGGAAGCCGCCCTCAAGAACCTTACCC
 CTTACAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCAACCTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCCAGACTGCCGGAC
 GAGGCCGACCACAGACG**TGAG**TCAGGTGAAAATGGAGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCAGCGCCACGCGCTCACTTCCAGGTCTCTCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGAGTACACCTTGG
 CATATGTTCTGTGTTTCACTAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAAAGSGPEGAGM
 TTVQTITGSDPEEAI FDTLCTDDSSSEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEGPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFPTSRD
 PLPSVPPTTNNSSRGNTSLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTCGCCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAAACATAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAAAT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTGCCAACGAGGAAGCCTGTCCATTGAACACAGCA
 AAAGGACTTATGAGTTACAGGATAAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCAACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGTCTGCCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCCTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACTGAACCACTGTCACTTCTC
 AGCCTCCACAGCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTACAGGCACTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCACTTCTCCAGGGCAGTGTTCAGAAAACTCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGTCTTTTGGTGTCTCTGCTTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
 TATTTTGAAGACAGGAAAAATGCCCCCTTCTGCTTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTGTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCCAACCTCCGCTC
 CTGGGTTCAAGCGATTCTCTCGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAAGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCCCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAATAGGTAAATTTGGGTAATCTGTCTCTAAAAATATAGCTAAAAACAAGCTCT
 ATGTAAGTAATAAAGTATAAATTGCCATATAAATTTCAAATTCACCTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
 TGTTTATCAATTTCTAATGGATTTGCTTTCTTTTATATGGATTCCTTTAAACCTTATT
 CCAGATGAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGTATGGGGTGCCTGCTGCT
 CCCAGGTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGTCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCCTTCTCTCGTGTCTTGGCACCATTCTATGCGAAGAAAGAGCCAGGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGTCTATTGTGACCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGTTCCAGGACCCTGCTGTCTCCCTCCCTTCTCCAC
 CTTCAGCCTCTGGCTACAACACGCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCCTCTGCAAGGAGCTCCCGCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAAG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTGCTGAGCCTTCTGTAGC
 CGCAGGCTGATGCCTTCTGTCAGCCACCTGCTCTGTGGAGAAAAGGACTCAACAGGCCA
 CGGAGACACAGAGAAACGAAAGTCTTGCTCTCAGCCTTGTACTGCGGAGGAAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCTCTTGCATGTTCAC
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAAGCGGTGGCCTTGCTCTTCCGGGTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC
 CTCATGCCCAGTGTGCGACCTGCCTTCTCCCACTCCAGACCCACCTTGCTCTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGTATGAAGAGGACATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTAAACAATGCCAGTGACTGTGCACTTGAGTTTGAAGGGCAGTGGGCGCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCTGTCTAAG
 TCCAGGCCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTTTTNNCCATTGGCCCTCCCTGGNCCATGCTTTTGGCTTTGGAAAAAATGATGAAGA
 AAACCTTGCTCTCTTCTGTCTGGAAGGGTTACTTGCTATGGGTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAAGAGTGCACGTAGGTGTCTAACACAGAGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACACTATTATTTTCTTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGCT
 TGTGCCAGGCTGGAGTGCAGTGGCAGCATCTGCAACTCCGCTCTGGGTCAAGTGATT
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTGGCCAGGCTGGTCTTGAACCTGCAC
 CTCAAATGAGCCTCTGCTTCACTCTCCAAATTCGGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTGAGTATGCAAAACCTGGAAG
 ATGAGGAGGAAAAAGAAAGAAAGAAAAAATGTACCCATAGTTCACCCAGAGACTATCAT
 TATTTCTGTTTGTGTACTTCTTCCACTCTTTTCTTCTTCCATTAATTGCGCGTGTCTTT
 TTTACAGAGCAATATCTTGTATATACACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAAGGTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDVTSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
TSQYGHERTSQYTGTSPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAAEKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128